(54) Title: NEW PRODUCTS SPECIFIC TO PATHOGENIC STRAINS AND THEIR USE AS VACCINES AND IN IMMUNOTHERAPY

(57) Abstract: The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of: 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria, 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates, 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates, 4- testing the polypeptides for immunogenicity using animals models. Application for making vaccines compositions and immunotherapies

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New products specific to pathogenic strains and their use as vaccines and in immunotherapy

The invention relates to new products specific to pathogenic strains, particularly to extra-intestinal *E. coli* strains.

It more particularly relates as products to antigenic polypeptides and antibodies directed against said polypeptides and to their use as vaccines and in immunotherapy, respectively.

Although *Escherichia coli* is probably the best known bacterial species and is one of the most common isolated in clinical microbiology laboratories, misconceptions abound regarding the various types of *E. coli* and the infections they cause.

E. coli strains of biological significance to humans can be broadly classified in 3 major groups:

1. Commensal strains, which are part of the normal flora.

2. Intestinal pathogenic strains, which are not part of the normal flora. This group contains various pathotypes (EPEC, EHEC, ETEC, EIEC) not including *Shigella*.

3. Extra-intestinal strains (ExPEC) which are responsible for infections outside the gastro-intestinal (GI) tract, but can also be part of the normal flora. All hosts, either immunocompromised or not are susceptible to these infections.

ExPEC strains are responsible for the majority of the urinary tract infections (UTI) particularly cystitis, pyelonephritis, and cathether associated infections.

They are also responsible for abdominal infections, nosocomial pneumoniae, neonatal meningitidis, soft tissue infections, and bone infections. Each one of these localizations can lead to

bacteremia with a risk of sepsis in case of organ failure. ExPEC strains are indeed the most common Gram negative bacilli isolated from blood cultures.

5   750 000 cases of bacterial sepsis occur each year in the US, and are responsible for 225 000 deaths. In a recent study on 1690 cases of sepsis, it was shown that the main bacteria species identified is ExPEC (16% of the cases) and then *S.aureus* (14% of the cases).

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These numbers demonstrate the importance of ExPEC strains in both hospital and community acquired infections.

ExPEC strains correspond to a homogenous subset of *E. coli*
15   strains. Analysis of phylogenetic relationships among *E. coli* strains by MLEE has revealed that *E. coli* belong to 4 main phylogenetic groups designated A, B1, B2 and D.

The pathogenesis of ExPEC strains is that of extra-cellular
20   microorganisms, i.e., they are well adapted to growth in the extra-cellular fluids and efficiently resist phagocytosis by polymorphonuclear. Initial studies have shown that virulence factors known to be important for the extra-cellular growth are mainly found in B2/D *E. coli.*, thus suggesting that B2/D
25   subgroups contain most of the ExPEC strains. This was reinforced by experiments performed on animals showing that B2/D strains are more virulent than A and B1 strains. Subsequent epidemiological studies have indeed confirmed these hypotheses. B2/D isolates are those predominantly responsible
30   for neonatal meningitidis (87%) and community or nosocomial acquired urosepsis, (93 % and 85%, respectively).

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Similar results have been reported for cystitis (70% are due
to the sole B2 E. coli), thus demonstrating that the
importance of ExPEC strains.

5   These recent findings demonstrate that the B2/D subgroup of
strains is the E. coli core genome the best adapted to growth
in extra-cellular fluids.

In addition to this core genome, ExPEC strains have various
10   pathogenicity islands which encode virulence factors
associated with the different pathogenesis of extra-intestinal
E. coli infections (UTI, urosepsis, neonatal meningitidis…).
Among the main virulence factors are the capsule, which is
well-known to be important for extra-cellular growth, and the
15   iron chelation systems (aerobactin and enterochelin, for
example). In addition, depending on the pathogenesis, these
strains can produce toxins (CNF, hemolysin…), adhesins (pap,
sfa…) and other iron chelation systems.

20   The notion that B2/D E. coli correspond to a distinct subset
of pathogenic E. coli strains is reinforced by the fact that
B2/D E. coli are not broadly isolated from the stools of
humans. They were recovered from only 11% of individuals,
whereas A and B1 subgroups are present in the stools of 74% of
25   the individuals of a human population.

As mentioned above the pathogenesis of ExPEC strains relies
on their ability to multiply in the extra-cellular fluids and
to resist bactericidal activity of the complement and
30   phagocytosis by polymorphonuclear. Therefore, as for other
extra-cellular pathogens (Haemophilus influenzae,
Streptococcus pneumonieae and Neisseria meningitidis) a
protective antigen against ExPEC has to induce antibodies

that promote opsonisation and/or the bactericidal activity of
serum.

Considering the above statements, an efficient antigen has to
5   be largely represented among the population of B2/D *E. coli*.
Similarly to other extra-cellular pathogens, the capsular
polysaccharide would be an ideal antigen, however most
pathogenic B2 strains express the K1 polysaccharide. The
latter has a structure identical to that of group B
10 meningococcus, which is non-immunogenic and shares common
antigens with the brain. Another possible target may be the
lipopolysaccharide (LPS). However there are a large number of
different LPS serotypes that are shared by various subgroups.

15 The inventors have now found that some specific components
coded by the B2/D genome, but absent from A and B1 *E. coli*
strains, are particularly useful as antigens and can
specifically prevent the pathologies due to ExPEC strains.
Homologs of these antigenic components can be found in other
20 pathogenic bacterial species and therefore are useful to
prevent the pathologies caused by these bacteria. Accordingly,
any reference to products specific to ExPEC strains and to
their uses will encompass components in these species.

25. For example homologuous antigens could be present in the
following species and be as such used for prevention of
disease due to the bacteria:

Pseudomonas aeruginosa, *Escherichia coli* O157:H7,*Yersinia*
30 *pestis*, *Vibrio cholerae*, *Legionella pneumophila*, *Salmonella*
enterica, *Salmonella typhimurium*, *Haemophilus influenzae*,
Neisseria meningitidis, *Neisseria gonorrhoeae*,
Bacillus anthracis, *Burkholderia cepacia*, *Campylobacter*
jejuni, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,

Clostridium botulinum, Clostridium difficile, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Helicobacter pylori, Klebsiella pneumoniae, Mycobacterium leprae, Mycobacterium tuberculosis, Pseudomonas aeruginosa,

5 *Salmonella paratyphi, Salmonella typhi, Staphylococcus aureus, Klebsiella pneumoniae, Listeria monocytogenes, Moxarella catarrhalis, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae,* and any species falling within the genera of any of the above

10 species.

It is then an object of the invention to provide new isolated antigenic polypeptides, and polynucleotides belonging to the core B2/D genome and not present in commensal *E. coli.*

15

Another object of the invention is to provide antibodies raised against such antigenic polypeptides, or peptidic fragments.

20 It is still another object of the invention to provide vectors and host cells containing said polynucleotides.

Another object of the invention is to provide vaccine compositions specific to extra intestinal infections caused by

25 ExPEC and pathologies caused by other pathogenic strains expressing antigenic polypeptides homologous to the ExPEC antigenic polypeptides.

The invention also relates to means for detecting and treating

30 a development of *E. coli* in a human or animal compartment which is extra-intestinal (systemic and non-diarrhoeal infections, such as septicaemia, pyelonephritis, or meningitis in the newborn).

The isolated antigenic polypeptides used according to the invention are selected among polypeptides specific to B2/D *E. coli* strains and not present in A and B1 isolates of *E. coli*. They are encoded by genes belonging to the core B2/D genome
5 and are not present in commensal *E. coli*.

They have a sequence selected in the group comprising the sequences of SEQ ID N°11 to N°66 or 133-145 or homologous sequences with a minimum of 25% of identity with the whole
10 sequences SEQ ID N°11 to N°66, or 133-145, respectively.

The isolated polypeptides having SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138 are new polypeptides and therefore are
15 part of the invention.

The invention also relates to homologous isolated antigenic peptides, comprising polypeptides having at least 25% identity to a polypeptide having a sequence SEQ ID N° as above
20 defined, more particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60
25 consecutive amino acids of a polypeptide having a sequence corresponding to said SEQ ID N°s, as determined using BLASTP or BLASTX with the default parameters.

Said polypeptides are obtainable by a process comprising the
30 steps of :
    a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,

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b- identifying the genes coding for said polypeptides which
    are conserved in B2/D clinical isolates,

c- purifying the polypeptides identified in step a, which
    are found in step 2 to be conserved in the B2/D isolates,

5   d- testing the polypeptides for immunogenicity using animals
        models.

By the term "conserved", it is meant, according to the
invention, that the genes coding for the polypeptides are
10 present with a frequency of at least 50% in B2/D isolates,
preferably greater than 60%, more preferably greater than 80%
and even more preferably greater than 85%, and in less than
40% in A/B isolates, preferably in less than 20%, more
preferably in less than 15%.

15

The animal models used in step c are infected adult animals,
eventually immunodepressed.

The adult animals particularly mice, are infected
20 intraperitoneally, the endpoint being the animal death and/or
bacteremia measurement.

The animals can be immunodepressed by injection, for example,
of cyclophosphamide which induces a neutropenia. Such a model
25 will validate the use of the antigen for prevention of E. coli
sepsis in immunodepressed patients. Another animal model could
be for example 2 to 3 day old infant mice.

The variants or fractionnal sequences conserving the B2/D
30 properties and which are antigenic as defined in step 4 of the
above process are also part of the invention. The term
"variant" is herein intended to mean any sequence having
insertions and/or deletions and/or substitutions with respect

to the parent sequence. The term "fractional" is herein intended to mean any fragment of the parent sequence.

The invention also relates to the use of isolated
5 polynucleotides coding for a polypeptide such as above defined according to the universal genetic code and taking into account the degeneracy of this code. The term "polynucleotide" encompasses any nucleotidic sequence such as DNA, including cDNA, RNA, including mRNA.
10

Said polynucleotides have preferably sequences corresponding to SEQ ID N°77 to SEQ ID N°132 or 146 to 158 .

More preferably, said polynucleotides have sequences
15 corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

The invention also relates to the homologs to said
20 polynucleotides . Said homologs may have at least 25% identity to a polynucleotide having said sequences, or at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a
25 polynucleotide having one of said SEQ ID N°s, as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.
30

The present application is also aimed towards any vector comprising at least one of said polynucleotides and also any cell transformed by genetic engineering, characterized in that it comprises, by transfection, at least one of said

polynucleotides and/or at least one vector according to the invention, and/or in that said transformation induces the production by this cell of at least one polypeptide corresponding to a polynucleotide such as above-defined.

5

The invention also relates to a process for isolating and identifying antigenic polypeptides, therefore useful as vaccine for *E. coli*.

10   Such a process comprises the steps of

        a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
15   b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
        c- purifying the polypeptides identified in step a, which are found in step 2 to be conserved in B2/D isolates,
        d- testing the polypeptides for immunogenicity using animals
20   models.

The selected antigenic polypeptides, alone or in combination, are capable of inducing an antibody response for prevention of infections due to ExPEC strains regardless of the pathogenesis
25   and of the infection site (UTI, pyelonephritis, sepsis, bacteremia, neonatal meningitis).

Such polypeptides particularly have sequences SEQ ID N°1 to SEQ ID N°66, or 133-145 or correspond to homologous sequences.
30

The invention thus relates to vaccine compositions specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide or fragment thereof as above defined, with a carrier, particularly at

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least one polypeptide of SEQ ID N°1 to SEQ ID N°66, except SEQ ID N°8, and 133-145 and the homologous polypeptides.

Such vaccine compositions are particularly useful for
5   preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.

The vaccine compositions of the invention are indicated for :
      - immunodepressed patients, ideally before the start of
10 the immunosuppressive therapy : patients suffering from cancer, diabetes, leukaemia, transplant patients, patients receiving long-term steroids therapy.
      - Patients before surgery where there is a high risk of
         E. coli infections (abdominal surgery).
15   - In all these cases, the E. coli vaccine of the
         invention could be administered in association with a
         Staphylococcus aureus vaccine,
      - Patients with recurrent UTI, especially after one
         episode of pyelonephritis.
20   - The prevention of neonatal infections will require
         vaccination of the mother, implying vaccination long
         before pregnancy to avoid potential problem. Ideally
         such a vaccine should be associated with a Group B
         Streptococcus polysaccharide vaccine in order to also
25   prevent late onset neonatal infections. It should be
         pointed out that the induction of a level of antibodies
         against B2/D E. coli in pregnant women would also
         prevent UTI, which are always a risk in the context of
         a pregnancy.
30

The formulation and the dose of said vaccine compositions can be developped and adjusted by those skilled in the art as a function of the indication targeted, of the method of

administration desired, and of the patient under consideration (age, weight).

These compositions comprise one or more physiologically inert
5   vehicles, and in particular any excipient suitable for the formulation and/or for the method of administration desired.

For example the vaccine could be a suspension of the purified polypeptide in sterile water with aluminium based miniral salt
10 as adjuvant and be administred subcutanously with a first and boosting injection.

The   antibodies   raised   against   the   above-identified polypeptides are also part of the invention.
15

They   are   capable   of   binding   to   said   polypeptides   in physiological-type conditions (*in vivo* or mimicking *in vivo*) when administered to a human or animal organism, and ELISA-type conditions when said binding product is intended to be
20 used   in   assays   and   methods   *in vitro*.   Such   antibodies advantageously inhibit the extra-intestinal growth of ExPEX strains in human or animal.

They are particularly useful for immunotherapy applications
25 with antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody (Mab) will be derived from the peptides or
30 polypeptides.

The methods for manufacturing such antibodies using the polypeptides according to the invention are available to those skilled in the art. They are conventional methods which

comprise, in particular, the immunization of animals such as rabbits and the harvesting of the serum produced, followed optionally by the purification of the serum obtained. A technique suitable for the production of monoclonal antibodies
5   is that of Köhler and Milstein (Nature 1975, 256:495-497).

Said antibodies do not recognize the cells of the human or animal to which it is intended.

10 In particular for immunotherapy applications with monoclonal antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody will
15 be derived from the peptides or polypeptides.

The antibodies or fragments thereof are advantageoulsy humanized when intended for a human administration.

20 Alternatively, humanized Mab could be derived from murine or rat Mab specific of the antigen. These fully humanized Mab are constructed using conventional molecular techniques to graft complementarity-determining regions from the parent murine or rat antibacterial antibody into human IgG1 kappa heavy and
25 light-chain frameworks.

The present invention is also aimed towards the use, in an effective amount, of at least one of polypeptides having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-
30 44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, antibodies or polynucleotides for the diagnosis of the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection.

The detection of the presence or absence of such compounds can in particular be carried out by nucleotide hybridization, by PCR amplification or by detection of their polypeptide products. Detection of the presence of such compounds makes it
5   possible to conclude that a B2/D *E. coli* strain is present.

The invention also relates to pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least
10 one polypeptide as above defined, particularly having SEQ ID N°1-66 to 133-145, in combination with a pharmaceutically acceptable carrier.

Preferred pharmaceutical compositions comprise at least one
15 polypeptide having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138,

The present application is also aimed towards any use of a
20 polypeptide such as above defined for the manufacture of a composition, in particular of a pharmaceutical composition, intended to alleviate and/or to prevent and/or to treat an undesirable growth of *E. coli*, such as an *E. coli* infection, (for example systemic and non-diarrhoeal infections), the
25 presence of extra-intestinal *E. coli* or a sanitary contamination.

The present invention is illustrated by the examples which follow and which are given in a non limiting capacity and with
30 reference to figures 1 and 2, wherein
    - Figure 1 represents a protein purification result after cloning and expression, and

- Figure 2 is a picture of the DNA array after hybridization with the genomic DNA from a B2/D reference strain.

5 **Example 1**: Assay for the immunogenicity of a selected polypeptide from sequences 1-66 and 133-145 (except SEQ ID N°8)

.   Cloning expression and purification of the selected
10 polypeptide.

The nucleic acid having SEQ ID N°95 encoding the polypeptide corresponding to SEQ ID N°28 was cloned without the signal sequence (coding the 16 first amino acids) in a prokaryotic
15 expression vector according to classical methods for cloning. The recombinant plasmid was used to transform the *E. coli* strain BL21. Transformed cells containing the recombinant plasmid were selected in LB medium with 100μg/ml ampicillin. Individual clones are picked and grown in presence of IPTG 1mM
20 to induce recombinant protein expression. Total protein content of the culture cells was extracted by cell lysis. Recombinant protein was purified by affinity columns.

Protein purification after cloning and expression
25

Total cell lysat of IPTG-induced bacteria were mixed with Ni-NTA matrix (Qiagen®) for 60 min et 4°C and loaded into a column. After washing the column to remove non specific binding, the recombinant protein was eluate 3 times with 1 ml
30 elution buffer pH 5.9. The protein was then eluate 4 times with 1 ml elution buffer pH 4.5.

Figure 1 represents a Coomassie blue stained SDS gel of recombinant protein after affinity column purification: **PM**:

14

markers   E1-4:   sample   collected   from   each   purification
fraction.   Arrow   indicate   the   band   corresponding   to   the
recombinant protein.

5   . Test for immunogenicity in an animal model

Polypeptide preparation from SEQ ID N°28 was injected to Swiss
mice to induce an antibody response as follows :

10   At d0 a first immunisation was done by injecting 20μg of the
protein at in 100μg solution of PBS and complet Freund
adjuvant (1:1). Control animals were injected with 100μl
solution of PBS and complet Freund adjuvant (1:1).

15   Boosting injection at d21 with 10μg of protein in 100μl PBS
and complet Freund adjuvant (1:1).

Sera from vaccinated animals was prepared from blood drawn by
puncture in the tail of the mice.
20

Detection of specific antibodies in animal sera, at d20 before
the boosting injection, was performed by western blot
according to standart protocol. Purified polypeptide was
subjected to electrophoresis (10μg per lane) and transfert to
25   nitrocellulose membrane.

The membranes were then saturated by incubation 35 min with
PBS/Tween20 0.1%/powder milk 5%.

30   Diluted sera was incubated with the membrane for 45 min.
Membranes were washed three time 5 min with PBS/tween. Bound
antibodies were then recognized by an anti-mouse IgG coupled
to horseradish peroxidase enzyme. After washing 3 times with
PBS/Tween and 3 time with PBS, enzymatic activity was revealed

by addition of chromogenic substrate DAB and hydrogen peroxyde.

Results : Sera from vaccinated animal, diluted at 1/100 revealed a unique band corresponding to the injected polypeptide. No antibody to the polypeptide could be detected in sera from control animals.

At d42, 300 μl of cyclophosphamide and 200μl at d45 were injected IP in the mice to induce neutropenia in order to increase the susceptibility to the challenge infection.
At d46 vaccinated and control mice were challenged by intraperitoneal injection of the wt B2/D strain C5 of *E. coli* at a dose equal to 10 time the LD50 (letal dose).

Immunogenicity of the selected polypeptide and protection conferred by vaccination with the seleted polypeptide was assessed by the survival of vaccinated animals three days post challenge.

Another example of vaccination to demonstrate immunogenicity of polypeptides:

- 24 Balb/c mice, female, 6 weeks old were immunized by subcutaneous Injection of the protein in Complete Freund's adjuvant, and 14 control mice were injected with CFA and PBS
- 3 weeks later a boost injection of 10 μg of protein in with incomplete Freund's adjuvant.

16

VACCINATION PROTOCOL

5

day 0	day 21	day 61	day 62

subcutaneous immunization
of mice (24) with 20 µg recombinant
proteinin 0,1ml solution with CFA

boost with 10 µg of
recombinant protein in
0,1 ml solution with IFA

blood sample collected from:
- 4 immunized mice
- 2 control mice

challenge
of mice

10

- analysis of antigen-specific
  antibody response (ELISA)
- WB on total bacterial lysat
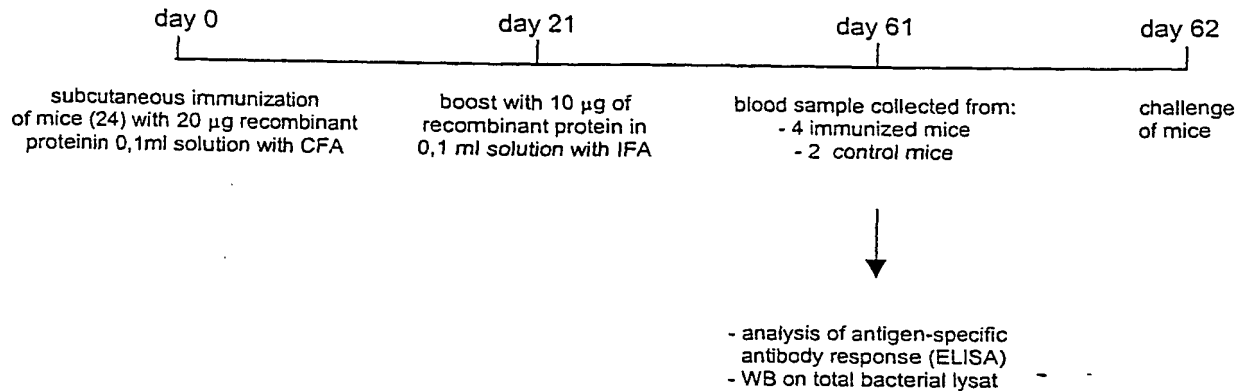
15   Before challenge at d62, sera was collected at d61 to analyze
the antibody response in the vaccinated animals.

- WB analysis of sera from immunized mice were performed to
  detect the antibody response to the recombinant proteine

20   used for immunization as described above.

- An ELISA assay was set up to measure antibody titer in
  vaccinated animals:

- Each recombinant protein was coated on a 96-well plates with

25   (200 ng/100 µl coating buffer), plates are saturat with
3%BSA in PBS.

- Twofold serial dilution of sera were made in PBS 1X/1% BSA
  from 1:500, to 1: 1024000 and incubated on the plate,
  antiboby binding was reavealed using a rabbit Anti-mouse IgG

30   conjugated with Peroxydase and OPD(o-phenylenediamine)
chromogen substrate.

- Read the OD_{495} with Sanofi Diagnostics Pasteur PR2100®

• Results:

Table 1. Sera titer against recombinant protein by ELISA

SEQ ID	serum1	serum 2	serum 3	serum 4	Control	recombinant protein
2	128	64	128	512	<0,5	
140	>64	>64	>64	>64	<0,5	+
31	>64	>64	>64	>64	<0,5	+
49	>64	>64	>64	>64	<0,5	+
51	>64	>64	>64	>64	<0,5	+
25	>64	>64	>64	>64	<0,5	+
7	16	8	>64	<0,5	<0,5	+
19	>64	>64	>64	>64	0,5	+
3	>64	>64	>64	>64	<0,5	+
26	512	128	64	256	<0,5	+
18	>64	>64	>64	>64	0,5	+
32	>64	>64	>64	>64	0,5	+
53	>64	>64	>64	>64	0,5	+
587	>64	16	32	32	<0,5	+
11	>64	32	32	64	<0,5	+
36	512	256	512	256	<0,5	+
10	32	128	256	128	0,5	+
47	512	512	512	512	0,5	+
20	1024	256	256	512	<0,5	+
17	1024	512	128	512	<0,5	+

5

• To assess the ability of sera to recognize the native
antigen expressed by the bacteria, western blot was also
performed on whole bacteria lysat.

10   To this end, bacteria were grown in LB medium supplemented or
not with iron chelator until OD600=0.5-0.6 and pelleted by
centrifugation 5 minutes at 10000 rpm. The pellet was lysed by
resuspension in 1X loading buffer containing SDS and heated 5
min at 95°C before migration on the gel.Western blot assay was
15   then performed with sera from controls and vaccinated animals.

Results in table 2 shows the results obtained with Sera from vaccinated mice against recombinant protein and against *E.coli* lysat.

5   Table 2: reactivity in Western Blot of sera from mice vaccinated with polypeptides encoded by the different ORFs

SEQ ID N°	whole cell lysate	recombinant protein
2	+	+
140	+	+
26	+	+

10   • Protection assay, end point: mortality

At d62, 20 vaccinated and 10 control mice were challenged with an *E.coli* virulent strain belonging to B2 group at a dose equal to the LD 50 (5.10^5 cfu/mice) by intraperitoneal
15   injection. Mortality is recorded at 48h, results in Table 3 are expressed as a percentage of protection representing the difference of survival in vaccinated versus control mice goups.

20   Table 3 : Protection obtained in mice challenged after immunization with proteines encoded by the corresponding ORFs.

SEQ ID N°	% protection
2	52
26	66
36	46
10	30
47	60
20	25

     • Protection assay, end point: bacteremia

30   At d62, 10 vaccinated and 5 control mice were challenged with an Ecoli virulent strain belonging to B2 group at a dose equal to the 1/5 of the LD 50 (1.10^5 cfu/mice) by intraperitoneal

injection.With this infectious dose the mice survived the infection at d48. At 48h blood was collected for each mice in presence of heparin .To assess bacteremia , the blood was plated on LB media and colonies count measured after overnight

5   culture.

     Example 2: Distribution of the DNA sequence of ORFs specific for B2/D group of E.coli in clinical isolates.

10   To make a DNA arrays membrane specific for B2/D group of E.coli , DNA corresponding to ORFs that were identified as specific for B2/D core genome of E.coli was amplified by PCR and spotted on nylon membrane using standard methods to those skilled in the art.

15

     Chromosomal DNA from 30 E.coli clinical isolate strains (of which 23 were from pathological conditions and 6 isolated from human normal flora), was prepared and radiolabelled with 33P.

20

     DNA from these clinical isolates was then hybridized to the B2/D specific DNA array, the results were read by a phosphoimager and spots reactivity was analyzed with an image analysis software. If hybridization gave a positive signal

25   for a particular ORF, this ORf is considered to be present in the genome of the isolate. Quality control of the array is the hybridization of a probe DNA from a reference strain of E.coli as shown in figure 2, which represents a picture of the DNA array after hybridization with the genomic DNA from a B2/D

30   reference strain.

The details of the method used for these experiments has been described previously in Tinsley et al. Methods Enzymol. 2002, 358; 188-207.

5   Results presented in Table 4 are expressed as the frequency of each ORF detection in the three different group A, B and D of *E.coli* strains.

10   Table 4 :Presence of Orfs encoding antigens in *E.coli* clinical isolate genomes

Frequency of positive signal %	Clinical isolate groups		
	A	D	B2
SEQ ID N°	N=6	n=5	n=18
86	17	20	100
119	0	80	100
137	0	0	100
77	0	100	94
78	0	100	100
79	0	100	100
80	0	0	100
84	0	0	100
82	0	0	100
88	0	0	100
83	0	0	94
85	0	0	78
88	0	0	56
81	33	20	100
89	33	60	67
90	0	0	61
91	17	80	67
94	0	0	100
92	0	0	100
93	0	0	100

96	0	100	100
85	17	100	100
97	0	70	100
98	0	0	100
99	0	0	78
101	0	80	100
102	0	0	100
104	0	0	11
103	0	0	100
105	0	0	67
100	0	100	100
111	17	0	61
115	0	0	78
114	0	0	83
113	0	0	94
120	33	80	16
125	17	0	89
109	0	0	33
110	0	0	17
124	0	0	72
126	0	80	78
116	0	0	33
112	0	0	22
106	17	0	33
117	33	80	11
132	33	80	22
122	0	0	22
74	0	0	89
70	0	0	33
73	0	0	89
71	50	100	22
75	0	0	0
76	0	0	56
67	0	0	50

69	100	100	100
68	67	100	100
152	0	0	94
153	0	100	100
150	0	0	11
142	83	100	78
157	67	0	94
156	17	100	100
100	0	100	100
154	0	80	67
147	0	0	100
146	17	100	100
158	17	100	89
107	17	0	78
72	50	100	44
151	0	0	11
149	0	0	28
148	0	0	6

Example 3 : Vaccines compositions intended for prevention of any form of infection by ExPEC.

5   The polypeptide coded by a sequence comprising SEQ ID N°28 is conjugated with a toxin and added to a physiologically inert vehicle.

This conjugated peptide is optionnally added to a childhood

10   vaccine.

The composition is sterilized and can be injected parenterally, subcutaneously or intramuscularly.

15   Said composition can also be sprayed onto mucosa with the aid of a spray.

CLAIMS

1.The isolated polypeptides having SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138.

2- Isolated antigenic polypeptides according to claim 1 obtainable by a process comprising the steps of :

a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,

b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,

c- purifying the polypeptides identified in step a, which are found in step b to be conserved in B2/D isolates,

d- testing the polypeptides for immunogenicity using animals models.

3. Isolated polynucleotides, coding for a polypeptide according to claim 1 or 2, according to the universal genetic code.

4. Isolated polynucleotides according to claim 3, having sequences selected in the group comprising SEQ ID N° 80, 81, 83, 87-89, 94-96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

5. An expression vector comprising at least an isolated polynucleotide according to claim 3 or 4.

6. A host cell comprising an expression vector according to claim 5.

24

7.   A   process   for   isolating   and   identifying   antigenic
polypeptides, useful as vaccines comprising the steps of :
a- selecting on the basis of sequence analysis those of the
polypeptides which are either located in the outermembrane or
5   secreted by the bacteria,
b- identifying the genes coding for said polypeptides which
are conserved in B2/D clinical isolates,
c- purifying the polypeptides identified in step a, which are
found in step b to be conserved in B2/D isolates,
10   d- testing the polypeptides for immunogenicity using animals
models.

8. The process of claim 7, comprising the use of infected
adult   animals,   eventually   immunodepressed,   and   of   infant
15   animals as models for neonatal infections.

9. The use of at least one polypeptide or fragment of
these polypeptides selected in the group comprising SEQ ID N°1
to SEQ ID N°66 (except SEQ ID N°8), or 133-145 as antigens and
20   the homologous sequences.

10. A vaccine composition specific to *E. coli* extra-
intestinal infections, comprising an effective amount of at
least one antigenic polypeptide such as selected by the
25   process of claim 7, or according to claim 9, alone or in
combination, particularly at least one polypeptide having a
sequence selected in the group comprising SEQ ID N°1 to SEQ ID
N°66, or 133-145, except SEQ ID N°8 and the homologous
sequences, with a carrier.
30

11. The vaccine composition of claim 10 for preventing
urinary system infections, pyelonephritis, sepsis, bacteremia,
neonatal meningitidis.

12. The vaccine composition of claim 10 or 11, adapted to specific indication in combination with components directed against other bacteria, such as *S.aureus* or group B *Streptococcus*. Or other bacteria implicated in systemic
5 infections.

13. Antibodies or fragments thereof directed against a polypeptide such as used according to claim 9.

10 14. Monoclonal antibodies against epitopes of polypeptide and there use as pharmaceutical compound for treatment or prevention of severe infection due to Expec in neonates and patients at risk for such infections.

15   15. A method for detecting the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection, comprising the use of at least one polypeptide such as defined in claim 1 or 2 or a polynucleotide according to claim 3 or 4, or an antibody to
20 claim 13 or 14, said polypeptide(s) being optionally in combination with anyone of the polypeptides having SEQ ID N°1-66 to 133-145.

16. Pharmaceutical composition for alleviating and/or
25 preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide according to claim 9, in combination with a pharmaceutically acceptable carrier.

FIGURE 1

FIGURE 2

1
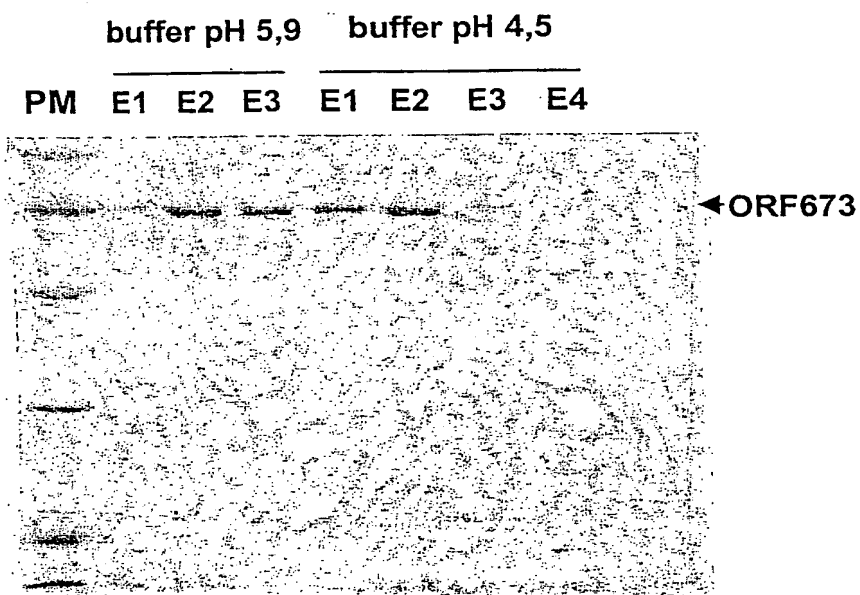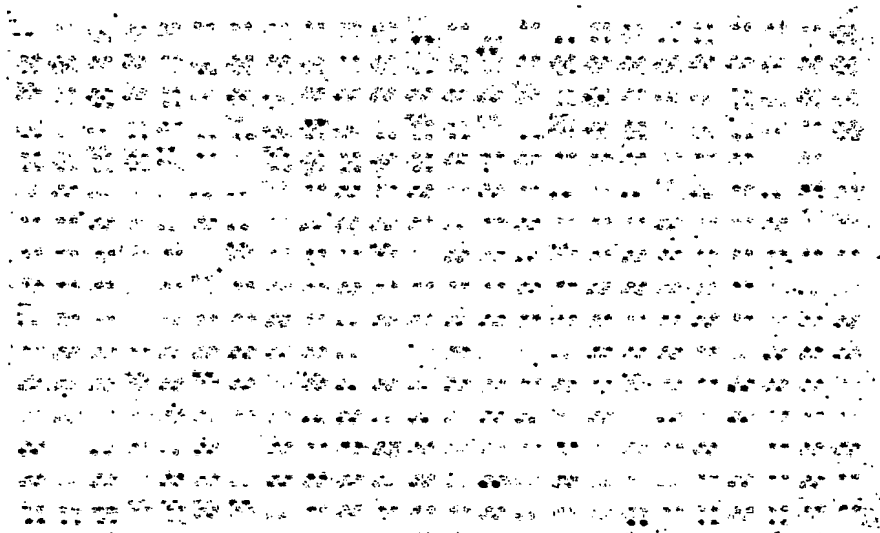
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1               5                   10                  15


Val Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Asn
            20                  25                  30


Val Leu Gln Arg Thr Cys Asn Val Pro Gly Asn Val Asp Val Ser Leu
        35                  40                  45


Gly Asn Leu Tyr Val Ser Asp Phe Pro Asn Ala Gly Ser Gly Ser Pro
    50                  55                  60


Trp Val Asn Phe Asp Leu Ser Leu Thr Gly Cys Gln Asn Met Asn Thr
65                  70                  75                  80


Val Arg Ala Thr Phe Ser Gly Thr Ala Asp Gly Gln Thr Tyr Tyr Ala
                85                  90                  95


Asn Thr Gly Asn Ala Gly Gly Ile Lys Ile Glu Ile Gln Asp Arg Asp
            100                 105                 110


Gly Ser Asn Ala Ser Tyr His Asn Gly Met Phe Lys Thr Leu Asn Val
        115                 120                 125


Gln Asn Asn Asn Ala Thr Phe Asn Leu Lys Ala Arg Ala Val Ser Lys
    130                 135                 140


Gly Gln Val Thr Pro Gly Asn Ile Ser Ser Val Ile Thr Val Thr Tyr
145                 150                 155                 160


Thr Tyr Ala
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1				5					10					15	

Met Lys Met Thr Arg Leu Tyr Pro Leu Ala Leu Gly Gly Leu Leu Leu
1   5   10   15

Pro Ala Ile Ala Asn Ala Gln Thr Ser Gln Gln Asp Glu Ser Thr Leu
          20   25   30

Val Val Thr Ala Ser Lys Gln Ser Ser Arg Ser Ala Ser Ala Asn Asn
          35   40   45

Val Ser Ser Thr Val Val Ser Ala Pro Glu Leu Ser Asp Ala Gly Val
     50   55   60

Thr Ala Ser Asp Lys Leu Pro Arg Val Leu Pro Gly Leu Asn Ile Glu
65   70   75   80

Asn Ser Gly Asn Met Leu Phe Ser Thr Ile Ser Leu Arg Gly Val Ser
               85   90   95

Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly
               100   105   110

Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln
          115   120   125

Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser
          130   135   140

Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr
145   150   155   160

Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg
               165   170   175

Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly
          180   185   190

Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro
          195   200   205

Ala Thr Gly Ser Asp Asp Leu Gly Gly Thr Arg Ala Ser Ile Gly Asn
    210   215   220

Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe
225   230   235   240

Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly
                245   250   255

Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro
                260   265   270

Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys
            275   280   285

Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln
    290   295   300

Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met
305   310   315   320

Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu
                325   330   335

Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn
            340   345   350

Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr
        355   360   365

Leu Ser Ser Thr Gly Tyr Thr Thr Ala Glu Thr Leu Ala Ala Tyr Ser
    370   375   380

Asp Leu Thr Trp His Leu Thr Asp Arg Phe Asp Ile Gly Gly Gly Val
385   390   395   400

Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu
                405   410   415

Gly Asn Pro Phe Gly Asp Gln Gly Lys Ser Asn Asp Asp Gln Val Leu
            420   425   430

4

Gly Gln Leu Ser Ala Gly Tyr Met Leu Thr Asp Asp Trp Arg Val Tyr
        435   440   445

Thr Arg Val Ala Gln Gly Tyr Lys Pro Ser Gly Tyr Asn Ile Val Pro
    450   455   460

Thr Ala Gly Leu Asp Ala Lys Pro Phe Val Ala Glu Lys Ser Ile Asn
465   470   475   480

Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala
                485   490   495

Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro
            500   505   510

Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly
        515   520   525

Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp
    530   535   540

Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu
545   550   555   560

Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser
            565   570   575

Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg
            580   585   590

Leu Ala Val Asn Leu Val Gly Pro His Tyr Phe Asp Gly Asp Asn Gln
        595   600   605

Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln
    610   615   620

Ala Thr Glu Arg Met Asn Ile Ser Val Tyr Val Asp Asn Leu Phe Asp
625   630   635   640

Arg Arg Tyr Arg Thr Tyr Gly Tyr Met Asn Gly Ser Ser Ala Val Ala
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Phe

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Gly Lys Ala Gly Ala Ser Val Met Ser Leu Ser Asp Gln Arg Phe Leu
        35   40   45

Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His
    50   55   60

Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro
65   70   75   80

Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly
                85   90   95

Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly
            100   105   110

Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met
        115   120   125

Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp
    130   135   140

Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly
145   150   155   160

Ile Ser Thr Trp Asp Tyr Glu Tyr Gly Ser Ser Gly Arg Glu Ser Leu
                165   170   175
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Ser Arg Ser Gly Ser Ala Asp Asn Phe Ala Trp Ser Leu Gly Ala Gly
　　　　　　　180　　　　　　　　　　185　　　　　　　　190

Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg
　　　　　195　　　　　　　　200　　　　　　　　205

Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly
　　　　210　　　　　　　　215　　　　　　　　220

Asp Lys Tyr Lys Ser Glu Val Asp Val Lys Ser His Asp Ile Met Leu
225　　　　　　　　　　230　　　　　　　　235　　　　　　　　240

Gly Met Thr Tyr Asn Phe
　　　　　　　　245

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Ala Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Arg
　　　　　　20　　　　　　　25　　　　　　　　30

Val Leu Pro Arg Thr Cys Thr Ile Gly Asn Gly Gly Asn Pro Asn Ala
　　　　35　　　　　　　40　　　　　　　　45

Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn
　　50　　　　　　　55　　　　　　　　60

Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln
65　　　　　　　70　　　　　　　75　　　　　　　　80

Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn
　　　　　　85　　　　　　　90　　　　　　　　95

Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln
　　　　　100　　　　　　　105　　　　　　　　110

Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val
　　　　115　　　　　　　120　　　　　　　125

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Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala
    130                 135                 140

Val Ser Lys Gly Asn Ala Gly Ala Gly Ser Ile Asn Ser Gln Ile Thr
145                 150                 155                 160

Val Thr Tyr Thr Tyr Ala
                165


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1               5                   10                  15

Ile Ala Val Ser Glu Leu Ala Lys Arg Val Ser Gly Lys Thr Asn Arg
            20                  25                  30

Lys Leu Val Ala Thr Met Leu Ser Leu Ala Val Ala Gly Thr Val Asn
        35                  40                  45

Ala Ala Asn Ile Asp Ile Ser Asn Val Trp Ala Arg Asp Tyr Leu Asp
    50                  55                  60

Leu Ala Gln Asn Lys Gly Ile Phe Gln Pro Gly Ala Thr Asp Val Thr
65                  70                  75                  80

Ile Thr Leu Lys Asn Gly Asp Lys Phe Ser Phe His Asn Leu Ser Ile
                85                  90                  95

Pro Asp Phe Ser Gly Ala Ala Ala Ser Gly Ala Ala Thr Ala Ile Gly
                100                 105                 110

Gly Ser Tyr Ser Val Thr Val Ala His Asn Lys Lys Asn Pro Gln Ala
            115                 120                 125

Ala Glu Thr Gln Val Tyr Ala Gln Ser Ser Tyr Arg Val Val Asp Arg
    130                 135                 140

Arg Asn Ser Asn Asp Phe Glu Ile Gln Arg Leu Asn Lys Phe Val Val
145                 150                 155                 160
```

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Glu Thr Val Gly Ala Thr Pro Ala Glu Thr Asn Pro Thr Thr Tyr Ser
              165             170             175

Asp Ala Leu Glu Arg Tyr Gly Ile Val Thr Ser Asp Gly Ser Lys Lys
              180             185             190

Ile Ile Gly Phe Arg Ala Gly Ser Gly Gly Thr Ser Phe Ile Asn Gly
              195             200             205

Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser
    210             215             220

Ala Ser Leu Phe Glu Val Thr Gln Trp Asp Ser Tyr Gly Met Met Ile
225             230             235             240

Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser
              245             250             255

Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu
              260             265             270

Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr
              275             280             285

Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr
    290             295             300

Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn
305             310             315             320

Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln
              325             330             335

Glu Lys Ile Thr Lys Asp Lys Asp Ile Val Phe Thr Asn Gly Gly Asp
              340             345             350

Val Leu Phe Lys Asp Asn Leu Asp Phe Gly Ser Gly Gly Ile Ile Phe
              355             360             365

Asp Glu Gly His Glu Tyr Asn Ile Asn Gly Gln Gly Phe Thr Phe Lys
              370             375             380
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Gly Ala Gly Ile Asp Ile Gly Lys Glu Ser Ile Val Asn Trp Asn Ala
385   390   395   400

Leu Tyr Ser Ser Asp Asp Val Leu His Lys Ile Gly Pro Gly Thr Leu
                405   410   415

Asn Val Gln Lys Lys Gln Gly Ala Asn Ile Lys Ile Gly Glu Gly Asn
            420   425   430

Val Ile Leu Asn Glu Glu Gly Thr Phe Asn Asn Ile Tyr Leu Ala Ser
        435   440   445

Gly Asn Gly Lys Val Ile Leu Asn Lys Asp Asn Ser Leu Gly Asn Asp
    450   455   460

Gln Tyr Ala Gly Ile Phe Phe Thr Lys Arg Gly Gly Thr Leu Asp Leu
465   470   475   480

Asn Gly His Asn Gln Thr Phe Thr Arg Ile Ala Ala Thr Asp Asp Gly
            485   490   495

Thr Thr Ile Thr Asn Ser Asp Thr Thr Lys Glu Ala Val Leu Ala Ile
        500   505   510

Asn Asn Glu Asp Ser Tyr Ile Tyr His Gly Asn Ile Asn Gly Asn Ile
    515   520   525

Lys Leu Thr His Asn Ile Asn Ser Gln Asp Lys Lys Thr Asn Ala Lys
    530   535   540

Leu Ile Leu Asp Gly Ser Val Asn Thr Lys Asn Asp Val Glu Val Ser
545   550   555   560

Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe
            565   570   575

Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp
        580   585   590

Trp Val Thr Val Leu Lys Glu Thr Glu Ser Ser Tyr Asn Lys Lys Phe
    595   600   605

Asn Ser Asp Tyr Lys Ser Asn Asn Gln Gln Thr Ser Phe Asp Gln Pro
    610   615   620

Asp Trp Lys Thr Gly Val Phe Lys Phe Asp Thr Leu His Leu Asn Asn
625   630   635   640

Ala Asp Phe Ser Ile Ser Arg Asn Ala Asn Val Glu Gly Asn Ile Ser
            645   650   655

Ala Asn Lys Ser Ala Ile Thr Ile Gly Asp Lys Asn Val Tyr Ile Asp
        660   665   670

Asn Leu Ala Gly Lys Asn Ile Thr Asn Asn Gly Phe Asp Phe Lys Gln
        675   680   685

Thr Ile Ser Thr Asn Leu Ser Ile Gly Glu Thr Lys Phe Thr Gly Gly
    690   695   700

Ile Thr Ala His Asn Ser Gln Ile Ala Ile Gly Asp Gln Ala Val Val
705   710   715   720

Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp
            725   730   735

Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly
        740   745   750

Ile Asp Ile Ser Gly Glu Leu Thr Met Met Gly Ile Pro Glu Gln Asn
        755   760   765

Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg
    770   775   780

Leu Ser Gly Gly Asn Ala Asn Phe Ile Ala Arg Asn Met Ala Ser Val
785   790   795   800

Thr Gly Asn Ile Tyr Ala Asp Asp Ala Ala Thr Ile Thr Leu Gly Gln
            805   810   815

Pro Glu Thr Glu Thr Pro Thr Ile Ser Ser Ala Tyr Gln Ala Trp Ala
            820   825   830

Glu Thr Leu Leu Tyr Gly Phe Asp Thr Ala Tyr Arg Gly Ala Ile Thr

```
                835                        840                        845

   Ala Pro Lys Ala Thr Val Ser Met Asn Asn Ala Ile Trp His Leu Asn
       850                     855                 860

   Ser Gln Ser Ser Ile Asn Arg Leu Glu Thr Lys Asp Ser Met Val Arg
   865                 870                 875                     880

   Phe Thr Gly Asp Asn Gly Lys Phe Thr Thr Leu Thr Val Asn Asn Leu
                   885                 890                     895

   Thr Ile Asp Asp Ser Ala Phe Val Leu Arg Ala Asn Leu Ala Gln Ala
                   900                 905                 910

   Asp Gln Leu Val Val Asn Lys Ser Leu Ser Gly Lys Asn Asn Leu Leu
           915                 920                 925

   Leu Val Asp Phe Ile Glu Lys Asn Gly Asn Ser Asn Gly Leu Asn Ile
       930                 935                 940

   Asp Leu Val Ser Ala Pro Lys Gly Thr Ala Val Asp Val Phe Lys Ala
   945                 950                 955                     960

   Thr Thr Arg Ser Ile Gly Phe Ser Asp Val Thr Pro Val Ile Glu Gln
                   965                 970                 975

   Lys Asn Asp Thr Asp Lys Ala Thr Trp Thr Leu Ile Gly Tyr Lys Ser
                   980                 985                 990

   Val Ala Asn Ala Asp Ala Ala Lys Lys Ala Thr Leu Leu Met Ser Gly
               995                 1000                1005

   Gly Tyr Lys Ala Phe Leu Ala Glu Val Asn Asn Leu Asn Lys Arg
       1010                1015                1020

   Met Gly Asp Leu Arg Asp Ile Asn Gly Glu Ser Gly Ala Trp Ala
       1025                1030                1035

   Arg Ile Ile Ser Gly Thr Gly Ser Ala Gly Gly Gly Phe Ser Asp
       1040                1045                1050

   Asn Tyr Thr His Val Gln Val Gly Ala Asp Asn Lys His Glu Leu
       1055                1060                1065
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Asp Gly Leu Asp Leu Phe Thr Gly Val Thr Met Thr Tyr Thr Asp
    1070   1075   1080

Ser His Ala Gly Ser Asp Ala Phe Ser Gly Glu Thr Lys Ser Val
    1085   1090   1095

Gly Ala Gly Leu Tyr Ala Ser Ala Met Phe Glu Ser Gly Ala Tyr
    1100   1105   1110

Ile Asp Leu Ile Gly Lys Tyr Val His His Asp Asn Glu Tyr Thr
    1115   1120   1125

Ala Thr Phe Ala Gly Leu Gly Thr Arg Asp Tyr Ser Ser His Ser
    1130   1135   1140

Trp Tyr Ala Gly Ala Glu Val Gly Tyr Arg Tyr His Val Thr Asp
    1145   1150   1155

Ser Ala Trp Ile Glu Pro Gln Ala Glu Leu Val Tyr Gly Ala Val
    1160   1165   1170

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr
    1175   1180   1185

Met Lys Asp Lys Asp Phe Asn Pro Leu Ile Gly Arg Thr Gly Val
    1190   1195   1200

Asp Val Gly Lys Ser Phe Ser Gly Lys Asp Trp Lys Val Thr Ala
    1205   1210   1215

Arg Ala Gly Leu Gly Tyr Gln Phe Asp Leu Phe Ala Asn Gly Glu
    1220   1225   1230

Thr Val Leu Arg Asp Ala Ser Gly Glu Lys Arg Ile Lys Gly Glu
    1235   1240   1245

Lys Asp Gly Arg Met Leu Met Asn Val Gly Leu Asn Ala Glu Ile
    1250   1255   1260

Arg Asp Asn Leu Arg Phe Gly Leu Glu Phe Glu Lys Ser Ala Phe
    1265   1270   1275

13

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Gly Lys  Tyr Asn Val Asp Asn  Ala Ile Asn Ala Asn  Phe Arg Tyr
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Ser Phe
    1295


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Met Ile Asn Ile Pro Ser Pro Thr Ala Val Val Met Ala Leu Val Ala
1                   5                   10                  15

Ile Ser Thr Leu Pro Ser Pro Ser Arg Val Lys Leu Met Pro Tyr Pro
                20                  25                  30

Pro Arg Ala His Asn Thr Thr Gly Leu Leu Pro Val Arg Glu Ile Cys
        35                  40                  45

Phe Pro His His Gly Asp Asp Gly Arg Asn Ser Ile Glu Pro Ser Ile
    50                  55                  60

Ser Arg Ala Ala His Thr Asp Arg Leu Arg Phe Val Cys Met Thr Arg
65                  70                  75                  80

Thr Gly Ser Thr Thr Ser Arg Pro Phe Cys Pro Ile Pro Arg Ser Pro
                85                  90                  95

Ala Leu Asn Ala Ser Gly Gln Gln Asp Ser Gly Phe Trp Gly Val Ser
            100                 105                 110

Ser Ile Pro Gly Asp Ile Leu Met Phe Gln Leu His Val Leu Ile Val
        115                 120                 125

Phe Ile Cys Lys Ile Asn Leu Ser Asp Asn Asn Ile Ser Tyr
    130                 135                 140

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            20   25   30

Lys Pro Asp Met Arg Pro Leu Gly Pro Asn Ile Ala Asp Lys Gly Ser
        35   40   45

Val Phe Tyr His Phe Ser Ala Thr Ser Phe Asp Ser Val Asp Gly Thr
    50   55   60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
65   70   75   80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
                85   90   95

Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro
            100   105   110

Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn
            115   120   125

Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
    130   135   140

Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
145   150   155   160

Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
            165   170   175

Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
            180   185   190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
    195   200   205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
    210   215   220

Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Thr Lys His Leu Ala

225   230   235   240

Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala
                    245   250   255

Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp
                    260   265   270

Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly
                    275   280   285

Pro Met Phe Asn Ala Ser Phe Arg Gln Ala Leu Leu Asp Ile Ser Gly
                    290   295   300

Glu Asn Ala Asn Tyr Thr Ala Gly Cys His Glu Leu Ser His
305   310   315

<210>   8
<211>   725
<212>   PRT
<213>   Escherichia coli
<400>   8

Met Arg Ile Asn Lys Ile Leu Trp Ser Leu Thr Val Leu Leu Val Gly
1   5   10   15

Leu Asn Ser Gln Val Ser Val Ala Lys Tyr Ser Asp Asp Asp Asn Asp
                    20   25   30

Glu Thr Leu Val Val Glu Ala Thr Ala Glu Gln Val Leu Lys Gln Gln
                    35   40   45

Pro Gly Val Ser Val Ile Thr Ser Glu Asp Ile Lys Lys Thr Pro Pro
        50   55   60

Val Asn Asp Leu Ser Asp Ile Ile Arg Lys Met Pro Gly Val Asn Leu
65   70   75   80

Thr Gly Asn Ser Ala Ser Gly Thr Arg Gly Asn Asn Arg Gln Ile Asp
                    85   90   95

Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Ile Asp Gly Val
                    100   105   110

16

Pro Val Thr Ser Arg Asn Ser Val Arg Tyr Ser Trp Arg Gly Glu Arg
    115   120   125

Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg
    130   135   140

Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala
145   150   155   160

Ala Gly Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asn Asp Trp
          165   170   175

His Gly Ser Leu Ser Leu Tyr Thr Asn Gln Pro Glu Ser Ser Glu Glu
        180   185   190

Gly Ala Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Ala Gly
      195   200   205

Asp Ala Leu Thr Thr Arg Leu Tyr Gly Asn Leu Asn Lys Thr Asp Ala
    210   215   220

Asp Ser Trp Asp Ile Asn Ser Pro Val Gly Thr Lys Asn Ala Ala Gly
225   230   235   240

His Glu Gly Val Arg Asn Lys Asp Ile Asn Gly Val Val Ser Trp Lys
          245   250   255

Leu Asn Pro Gln Gln Ile Leu Asp Phe Glu Val Gly Tyr Ser Arg Gln
        260   265   270

Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Ser Ser Ser Ser Ala Val
      275   280   285

Thr Glu Ser Leu Ala Lys Ser Gly Lys Glu Thr Asn Arg Leu Tyr Arg
    290   295   300

Gln Asn Tyr Gly Ile Thr His Asn Gly Ile Trp Asp Trp Gly Gln Ser
305   310   315   320

Arg Phe Gly Val Tyr Tyr Glu Lys Thr Asn Asn Thr Arg Met Asn Glu
        325   330   335

Gly Leu Ser Gly Gly Gly Glu Gly Arg Ile Leu Ala Gly Glu Lys Phe

17

```
              340                345                350

Thr Thr Asn Arg Leu Ser Ser Trp Arg Thr Ser Gly Glu Leu Asn Ile
        355                360                365


Pro Leu Asn Val Met Val Asp Gln Thr Leu Thr Val Gly Ala Glu Trp
    370                375                380


Asn Arg Asp Lys Leu Asp Asp Pro Ser Ser Thr Ser Leu Thr Val Asn
385                390                395                400


Asp Arg Asp Ile Ser Gly Ile Ser Gly Ser Ala Ala Asp Arg Ser Ser
                405                410                415


Lys Asn His Ser Gln Ile Ser Ala Leu Tyr Ile Glu Asp Asn Ile Glu
            420                425                430


Pro Val Pro Gly Thr Asn Ile Ile Pro Gly Leu Arg Phe Asp Tyr Leu
            435                440                445


Ser Asp Ser Gly Gly Asn Phe Ser Pro Ser Leu Asn Leu Ser Gln Glu
    450                455                460


Leu Gly Asp Tyr Phe Lys Val Lys Ala Gly Val Ala Arg Thr Phe Lys
465                470                475                480


Ala Pro Asn Leu Tyr Gln Ser Ser Glu Gly Tyr Leu Leu Tyr Ser Lys
                485                490                495


Gly Asn Gly Cys Pro Lys Asp Ile Thr Ser Gly Gly Cys Tyr Leu Ile
            500                505                510


Gly Asn Lys Asp Leu Asp Pro Glu Ile Ser Val Asn Lys Glu Ile Gly
        515                520                525


Leu Glu Phe Thr Trp Glu Asp Tyr His Ala Ser Val Thr Tyr Phe Arg
    530                535                540


Asn Asp Tyr Gln Asn Lys Ile Val Ala Gly Asp Asn Val Ile Gly Gln
545                550                555                560


Thr Ala Ser Gly Ala Tyr Ile Leu Lys Trp Gln Asn Gly Gly Lys Ala
            565                570                575
```

```
Leu Val Asp Gly Ile Glu Ala Ser Met Ser Phe Pro Leu Val Lys Glu
            580                 585                 590

Arg Leu Asn Trp Asn Thr Asn Ala Thr Trp Met Ile Thr Ser Glu Gln
            595                 600                 605

Lys Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Lys Tyr Thr Ile Asn
    610                 615                 620

Asn Ser Leu Asn Trp Thr Ile Thr Gln Ala Phe Ser Ala Ser Phe Asn
625                 630                 635                 640

Trp Thr Leu Tyr Gly Arg Gln Lys Pro Arg Thr His Ala Glu Thr Arg
                645                 650                 655

Ser Glu Asp Thr Gly Gly Leu Ser Gly Lys Glu Leu Gly Ala Tyr Ser
            660                 665                 670

Leu Val Gly Thr Asn Phe Asn Tyr Asp Ile Asn Lys Asn Leu Arg Leu
            675                 680                 685

Asn Val Gly Val Ser Asn Ile Leu Asn Lys Gln Ile Phe Arg Ser Ser
    690                 695                 700

Glu Gly Ala Asn Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Gly
705                 710                 715                 720

Val Thr Ala Ser Phe
                725


<210>   9
<211>   1014
<212>   PRT
<213>   Escherichia coli
<400>   9

Met Gly Asn Gln Trp Gln Gln Lys Tyr Leu Leu Glu Tyr Asn Glu Leu
1               5                   10                  15

Val Ser Asn Phe Pro Ser Pro Glu Arg Val Val Ser Asp Tyr Ile Lys
                20                  25                  30

Asn Cys Phe Lys Thr Asp Leu Pro Trp Phe Ser Arg Ile Asp Pro Asp
```

19

```
        35                    40                      45

Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser
    50                  55                  60

Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr
65                  70                  75                  80

Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe
                85                  90                  95

Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp
            100                 105                 110

Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu
        115                 120                 125

His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu
    130                 135                 140

Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys
145                 150                 155                 160

Asn Tyr Tyr Ile Ser Ser Ala Leu Tyr Leu Tyr Lys Asn Gly Glu Leu
            165                 170                 175

Asp Glu Arg Glu Tyr Asn Phe Ser Met Asn Ala Leu Asn Arg Ser Asp
            180                 185                 190

Asn Ile Ser Leu Leu Phe Phe Asp Ile Tyr Gly Tyr Tyr Ala Ser Asp
            195                 200                 205

Ile Phe Val Ala Lys Asn Asn Asp Lys Val Met Leu Phe Ile Pro Gly
    210                 215                 220

Ala Lys Lys Pro Phe Leu Phe Lys Lys Asn Ile Ala Asp Leu Arg Leu
225                 230                 235                 240

Thr Leu Lys Glu Leu Ile Lys Asp Ser Asp Asn Lys Gln Leu Leu Ser
            245                 250                 255

Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Val Ser Tyr Ala Gly
            260                 265                 270
```

Val Asn Ser Val Leu His Ala Ile Glu Asn Asp Gly Asn Phe Asn Glu
        275   280   285

Ser Tyr Phe Leu Tyr Ser Asn Lys Thr Leu Ser Asn Lys Asp Val Phe
        290   295   300

Asp Ala Ile Ala Ile Ser Val Lys Lys Arg Ser Phe Ser Asp Gly Asp
305   310   315   320

Ile Val Ile Lys Ser Asn Ser Glu Ala Gln Arg Asp Tyr Ala Leu Thr
                325   330   335

Ile Leu Gln Thr Ile Leu Ser Met Thr Pro Ile Phe Asp Ile Val Val
                340   345   350

Pro Glu Val Ser Val Pro Leu Gly Leu Gly Ile Ile Thr Ser Ser Met
        355   360   365

Gly Ile Ser Phe Asp Gln Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg
    370   375   380

Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Ala Val Leu Leu Gly Leu
385   390   395   400

Ser Phe Ala Ile Pro Leu Leu Ile Ser Lys Ala Gly Ile Asn Gln Glu
                405   410   415

Val Leu Ser Ser Val Ile Asn Asn Glu Gly Arg Thr Leu Asn Glu Thr
                420   425   430

Asn Ile Asp Ile Phe Leu Lys Glu Tyr Gly Ile Ala Glu Asp Ser Ile
        435   440   445

Ser Ser Thr Asn Leu Leu Asp Val Lys Leu Lys Ser Ser Gly Gln His
    450   455   460

Val Asn Ile Val Lys Leu Ser Asp Glu Asp Asn Gln Ile Val Ala Val
465   470   475   480

Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr
                485   490   495

Gly Tyr Glu Ile Leu Ser Arg Arg Ile Tyr Arg Thr Glu Tyr Asn Asn
        500   505   510

Glu Ile Leu Trp Thr Arg Gly Gly Gly Leu Lys Gly Gly Gln Pro Phe
        515   520   525

Asp Phe Glu Ser Leu Asn Ile Pro Val Phe Phe Lys Asp Glu Pro Tyr
        530   535   540

Ser Ala Val Thr Gly Ser Pro Leu Ser Phe Ile Asn Asp Asp Ser Ser
545   550   555   560

Leu Leu Tyr Pro Asp Thr Asn Pro Lys Leu Pro Gln Pro Thr Ser Glu
                565   570   575

Met Asp Ile Val Asn Tyr Val Lys Gly Ser Gly Ser Phe Gly Asp Arg
            580   585   590

Phe Val Thr Leu Met Arg Gly Ala Thr Glu Glu Glu Ala Trp Asn Ile
        595   600   605

Ala Ser Tyr His Thr Ala Gly Gly Ser Thr Glu Glu Leu His Glu Ile
    610   615   620

Leu Leu Gly Gln Gly Pro Gln Ser Ser Leu Gly Phe Thr Glu Tyr Thr
625   630   635   640

Ser Asn Val Asn Ser Ala Asp Ala Ala Ser Arg Arg His Phe Leu Val
                645   650   655

Val Ile Lys Val His Val Lys Tyr Ile Thr Asn Asn Asn Val Ser Tyr
            660   665   670

Val Asn His Trp Ala Ile Pro Asp Glu Ala Pro Val Glu Val Leu Ala
        675   680   685

Val Val Asp Arg Arg Phe Asn Phe Pro Glu Pro Ser Thr Pro Pro Asp
    690   695   700

Ile Ser Thr Ile Arg Lys Leu Leu Ser Leu Arg Tyr Phe Lys Glu Ser
705   710   715   720

22

Ile Glu Ser Thr Ser Lys Ser Asn Phe Gln Lys Leu Ser Arg Gly Asn
            725   730   735

Ile Asp Val Leu Lys Gly Arg Gly Ser Ile Ser Ser Thr Arg Gln Arg
            740   745   750

Ala Ile Tyr Pro Tyr Phe Glu Ala Ala Asn Ala Asp Glu Gln Gln Pro
            755   760   765

Leu Phe Phe Tyr Ile Lys Lys Asp Arg Phe Asp Asn His Gly Tyr Asp
            770   775   780

Gln Tyr Phe Tyr Asp Asn Thr Val Gly Leu Asn Gly Ile Pro Thr Leu
785   790   795   800

Asn Thr Tyr Thr Gly Glu Ile Pro Ser Asp Ser Ser Ser Leu Gly Ser
            805   810   815

Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg
            820   825   830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu
            835   840   845

Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser
850   855   860

Gly Cys Thr Thr Ile Val Ala Arg Lys Glu Gly Tyr Ile Tyr Lys Val
865   870   875   880

His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly
            885   890   895

Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile
            900   905   910

Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu
            915   920   925

Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys
            930   935   940

Lys Pro Asp Ser Gln Ile Thr Ile Ile Arg Asp Asn Val Ser Val Phe

945   950   955   960

Pro Tyr Phe Leu Asp Asn Ile Pro Glu His Gly Phe Gly Thr Ser Ala
              965   970   975

Thr Val Leu Val Arg Val Asp Gly Asn Val Val Val Arg Ser Leu Ser
              980   985   990

Glu Ser Tyr Ser Leu Asn Ala Asp Ala Ser Glu Ile Ser Val Leu Lys
          995   1000   1005

Val Phe Ser Lys Lys Phe
     1010

<210> 10
<211> 454
<212> PRT
<213> Escherichia coli
<400> 10

Met Val Asp Met Ile Asn Glu Ser Ala Arg Gln Thr Pro Val Ile Ala
1   5   10   15

Gln Thr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala
              20   25   30

Ala Ile Ala Ala Gly Arg Leu Gly Ala Arg Thr Met Ile Val Glu Arg
         35   40   45

Tyr Gly Ser Leu Gly Gly Val Leu Thr Gln Val Gly Val Glu Ser Phe
      50   55   60

Ala Trp Tyr Arg His Pro Gly Thr Glu Asp Cys Glu Gly Ile Cys Arg
65   70   75   80

Glu Tyr Glu Gly Arg Ala Arg Ala Leu Gly Phe Thr Arg Pro Glu Pro
              85   90   95

Gln Ser Ile Ser Glu Val Ile Asp Thr Glu Gly Phe Lys Val Val Ala
              100   105   110

Asp Gln Met Ile Thr Glu Ser Gly Val Glu Pro Leu Tyr His Ser Trp
         115   120   125

```
Val Val Asp Val Ile Lys Asp Gly Asp Thr Leu Cys Gly Val Ile Val
    130                 135                 140

Glu Asn Lys Ser Gly Arg Gly Ala Ile Leu Ala Lys Arg Ile Val Asp
145                 150                 155                 160

Cys Thr Gly Asp Ala Asp Ile Ala Ala Arg Ala Gly Ala Pro Trp Thr
                165                 170                 175

Lys Arg Ser Lys Asp Gln Leu Met Gly Val Thr Val Met Phe Ser Cys
            180                 185                 190

Ala Gly Val Asp Val Ala Arg Phe Asn Arg Phe Val Ala Glu Glu Leu
            195                 200                 205

Lys Pro Thr Tyr Ala Asp Trp Gly Lys Asn Trp Thr Ile Gln Thr Thr
    210                 215                 220

Gly Lys Glu Asp Pro Met Phe Ser Pro Tyr Met Glu Asp Ile Phe Thr
225                 230                 235                 240

Arg Ala Gln Gln Asp Gly Val Ile Pro Gly Asp Ala Gln Ala Ile Ala
                245                 250                 255

Gly Thr Trp Ser Thr Phe Ser Glu Ser Gly Glu Ala Phe Gln Met Asn
            260                 265                 270

Met Val Tyr Ala Phe Gly Phe Asp Cys Thr Asp Val Phe Asp Leu Thr
    275                 280                 285

Lys Ala Glu Ile Ala Gly Arg Gln Gln Ala Leu Trp Ala Ile Asp Ala
    290                 295                 300

Leu Arg His Tyr Val Pro Gly Phe Glu Asn Val Arg Leu Arg Asn Phe
305                 310                 315                 320

Gly Ala Thr Leu Gly Thr Arg Glu Ser Arg Leu Ile Glu Gly Glu Ile
            325                 330                 335

Arg Ile Ala Asp Asp Tyr Val Leu Asn Gln Gly Arg Cys Ser Asp Ser
            340                 345                 350

Val Gly Ile Phe Pro Glu Phe Ile Asp Gly Ser Gly Tyr Leu Ile Leu
```

```
          355                      360                      365

  Pro Thr Thr Gly Arg Phe Phe Gln Ile Pro Tyr Gly Cys Leu Val Pro
      370                  375              380

  Gln Lys Val Glu Asn Leu Leu Val Ala Gly Arg Cys Ile Ser Ala Gly
  385                  390              395                  400

  Val Val Ala His Thr Ser Met Arg Asn Met Met Cys Cys Ala Val Thr
              405              410              415

  Gly Glu Ala Ala Gly Thr Ala Ala Val Val Ser Leu Gln Gln Asn Cys
              420              425              430

  Thr Val Arg Gln Val Ala Ile Pro Asp Leu Gln Asn Thr Leu Gln Gln
          435              440              445

  Gln Gly Val Arg Leu Ala
      450


<210>   11
<211>   253
<212>   PRT
<213>   Escherichia coli
<400>   11

  Met Ser Ala Lys Arg Arg Leu Leu Ile Ala Cys Thr Leu Ile Thr Ala
  1               5                   10                  15

  Ile Tyr His Phe Pro Ala Tyr Ser Ser Leu Glu Tyr Lys Gly Thr Phe
              20                  25                  30

  Gly Ser Ile Asn Ala Gly Tyr Ala Asp Trp Asn Ser Gly Phe Val Asn
          35                  40                  45

  Thr His Arg Gly Glu Val Trp Lys Val Thr Ala Asp Phe Gly Val Asn
      50                  55                  60

  Phe Lys Glu Ala Glu Phe Tyr Ser Phe Tyr Glu Ser Asn Val Leu Asn
  65                  70                  75                  80

  His Ala Val Ala Gly Arg Asn His Thr Val Ser Ala Met Thr His Val
              85                  90                  95
```

26

Arg Leu Phe Asp Ser Asp Met Thr Phe Phe Gly Lys Ile Tyr Gly Gln
            100   105   110

Trp Asp Asn Ser Trp Gly Asp Asp Leu Asp Met Phe Tyr Gly Phe Gly
        115   120   125

Tyr Leu Gly Trp Asn Gly Glu Trp Gly Phe Phe Lys Pro Tyr Ile Gly
        130   135   140

Leu His Asn Gln Ser Gly Asp Tyr Val Ser Ala Lys Tyr Gly Gln Thr
145   150   155   160

Asn Gly Trp Asn Gly Tyr Val Val Gly Trp Thr Ala Val Leu Pro Phe
                    165   170   175

Thr Leu Phe Asp Glu Lys Phe Val Leu Ser Asn Trp Asn Glu Ile Glu
            180   185   190

Leu Asp Arg Asn Asp Ala Tyr Thr Glu Gln Gln Phe Gly Arg Asn Gly
            195   200   205

Leu Asn Gly Gly Leu Thr Ile Ala Trp Lys Phe Tyr Pro Arg Trp Lys
    210   215   220

Ala Ser Val Thr Trp Arg Tyr Phe Asp Asn Lys Leu Gly Tyr Asp Gly
225   230   235   240

Phe Gly Asp Gln Met Ile Tyr Met Leu Gly Tyr Asp Phe
                    245   250

<210> 12
<211> 492
<212> PRT
<213> Escherichia coli
<400> 12

Met Ala Ser Leu Ile Gly Leu Ala Val Cys Thr Gly Asn Ala Phe Ser
1   5   10   15

Pro Ala Leu Ala Ala Glu Ala Lys Gln Pro Asn Leu Val Ile Ile Met
            20   25   30

Ala Asp Asp Leu Gly Tyr Gly Asp Leu Ala Thr Tyr Gly His Gln Ile
        35   40   45

```
Val Lys Thr Pro Asn Ile Asp Arg Leu Ala Gln Glu Gly Val Lys Phe
    50                  55                  60

Thr Asp Tyr Tyr Ala Pro Ala Pro Leu Ser Ser Pro Ser Arg Ala Gly
65                  70                  75                  80

Leu Leu Thr Gly Arg Met Pro Phe Arg Thr Gly Ile Arg Ser Trp Ile
                85                  90                  95

Pro Ser Gly Lys Asp Val Ala Leu Gly Arg Asn Glu Leu Thr Ile Ala
                100                 105                 110

Asn Leu Leu Lys Ala Gln Gly Tyr Asp Thr Ala Met Met Gly Lys Leu
        115                 120                 125

His Leu Asn Ala Gly Gly Asp Arg Thr Asp Gln Pro Gln Ala Gln Asp
    130                 135                 140

Met Gly Phe Asp Tyr Ser Leu Ala Asn Thr Ala Gly Phe Val Thr Asp
145                 150                 155                 160

Ala Thr Leu Asp Asn Ala Lys Glu Arg Pro Arg Tyr Gly Met Val Tyr
                165                 170                 175

Pro Thr Gly Trp Leu Arg Asn Gly Gln Pro Thr Pro Arg Ala Asp Lys
                180                 185                 190

Met Ser Gly Glu Tyr Val Ser Ser Glu Val Val Asn Trp Leu Asp Asn
        195                 200                 205

Lys Lys Asp Ser Lys Pro Phe Phe Leu Tyr Val Ala Phe Thr Glu Val
    210                 215                 220

His Ser Pro Leu Ala Ser Pro Lys Lys Tyr Leu Asp Met Tyr Ser Gln
225                 230                 235                 240

Tyr Met Ser Ala Tyr Gln Lys Gln His Pro Asp Leu Phe Tyr Gly Asp
                245                 250                 255

Trp Ala Asp Lys Pro Trp Arg Gly Val Gly Glu Tyr Tyr Ala Asn Ile
                260                 265                 270
```

```
Ser Tyr Leu Asp Ala Gln Val Gly Lys Val Leu Asp Lys Ile Lys Ala
        275             280             285

Met Gly Glu Glu Asp Asn Thr Ile Val Ile Phe Thr Ser Asp Asn Gly
    290             295             300

Pro Val Thr Arg Glu Ala Arg Lys Val Tyr Glu Leu Asn Leu Ala Gly
305             310             315             320

Glu Thr Asp Gly Leu Arg Gly Arg Lys Asp Asn Leu Trp Glu Gly Gly
            325             330             335

Ile Arg Val Pro Ala Ile Ile Lys Tyr Gly Lys His Leu Pro Gln Gly
            340             345             350

Met Val Ser Asp Thr Pro Val Tyr Gly Leu Asp Trp Met Pro Thr Leu
        355             360             365

Ala Lys Met Met Asn Phe Lys Leu Pro Thr Asp Arg Thr Phe Asp Gly
    370             375             380

Glu Ser Leu Val Pro Val Leu Glu Gln Lys Ala Leu Lys Arg Glu Lys
385             390             395             400

Pro Leu Ile Phe Gly Ile Asp Met Pro Phe Gln Asp Asp Pro Thr Asp
            405             410             415

Glu Trp Ala Ile Arg Asp Gly Asp Trp Lys Met Ile Ile Asp Arg Asn
            420             425             430

Asn Lys Pro Lys Tyr Leu Tyr Asn Leu Lys Ser Asp Arg Tyr Glu Thr
        435             440             445

Leu Asn Leu Ile Gly Lys Lys Pro Asp Ile Glu Lys Gln Met Tyr Gly
    450             455             460

Lys Phe Leu Lys Tyr Lys Thr Asp Ile Asp Asn Asp Ser Leu Met Lys
465             470             475             480

Ala Arg Gly Asp Lys Pro Glu Ala Val Thr Trp Gly
            485             490
```

<210> 13

<211> 345
<212> PRT
<213> Escherichia coli
<400> 13

Leu Ile Ser Leu Ser Phe Ile Pro Val Met Ser Ala Leu Pro Gly Pro
1   5   10   15

Ile Ala Lys Gly Phe Arg Asn Glu Arg Gly Phe Val Thr Thr Thr Ile
                20   25   30

Cys Ala Met Gly Glu Leu Leu Ala Glu Phe Leu Ser Arg Asn Pro His
            35   40   45

Gln Lys Phe Thr Gln Pro Gly Glu Phe Ile Gly Pro Phe Pro Ser Gly
    50   55   60

Ala Pro Ala Ile Phe Ala Ala Gln Val Ala Lys Leu Ser His Arg Ala
65   70   75   80

Ile Phe Phe Gly Cys Val Gly Asn Asp Asp Phe Ala Arg Leu Ile Ile
            85   90   95

Glu Arg Leu Arg His Glu Gly Val Ile Thr Asp Gly Ile His Val Met
            100   105   110

Asn Asn Ala Val Thr Gly Thr Ala Phe Val Ser Tyr Gln Asn Pro Gln
        115   120   125

Gln Arg Asp Phe Val Phe Asn Ile Pro Asn Ser Ala Cys Gly Leu Phe
    130   135   140

Thr Ala Glu His Ile Asp Lys Asp Leu Leu Lys Gln Cys Asn His Leu
145   150   155   160

His Ile Val Gly Ser Ser Leu Phe Ser Phe Arg Met Ile Asp Val Met
                165   170   175

Arg Lys Ala Ile Thr Thr Ile Lys Ser Ala Gly Gly Thr Val Ser Phe
            180   185   190

Asp Pro Asn Ile Arg Lys Glu Met Leu Ser Ile Pro Glu Met Ala Gln
        195   200   205

```
Ala Leu Asp Tyr Leu Ile Glu Tyr Thr Asp Ile Phe Ile Pro Ser Glu
    210             215             220

Ser Glu Leu Pro Phe Phe Ala Arg His Lys Asn Leu Ser Glu Glu Gln
225             230             235             240

Ile Val Ser Asp Leu Leu His Gly Gly Val Lys His Val Ala Ile Lys
            245             250             255

Arg Ala Gln Arg Gly Ala Ser Tyr Tyr Lys Leu Lys Asn Gly Thr Leu
            260             265             270

His Ala Gln His Val Ala Gly His Asp Ile Glu Ile Ile Asp Pro Thr
        275             280             285

Gly Ala Gly Asp Cys Phe Gly Ala Thr Phe Ile Thr Leu Phe Leu Ser
    290             295             300

Gly Phe Pro Ala His Lys Ala Leu Gln Tyr Ala Asn Ala Ser Gly Ala
305             310             315             320

Leu Ala Val Met Arg Gln Gly Pro Met Glu Gly Ile Ser Ser Leu Ala
            325             330             335

Asp Ile Glu Asp Phe Leu Gln Gln His
            340             345


<210>  14
<211>  192
<212>  PRT
<213>  Escherichia coli
<400>  14

Met Tyr Met Pro Gly Lys Gln Met Leu Cys Cys Ile Leu Ile Ser Ile
1               5                   10              15

Ile Ser Glu Gly Asp Met Lys Ile Phe Ile Ser Leu Phe Leu Phe Ile
            20              25              30

Ile Ser Thr Asn Ser Phe Ala Asp Asp Ile Thr His Ala Gly Val Val
        35              40              45

Arg Ile Glu Gly Leu Ile Thr Glu Lys Thr Cys Ile Ile Ser Asp Glu
    50              55              60
```

```
Ser Lys Asn Phe Thr Val Asn Met Pro Asp Val Pro Ser Ser Ser Val
65                  70              75              80


Arg Ser Ala Gly Asp Val Thr Glu Lys Val Tyr Phe Ser Ile Thr Leu
                85              90              95


Thr Arg Cys Gly Ser Asp Val Gly Asn Ala Tyr Ile Lys Phe Thr Gly
            100             105             110


Asn Thr Val Ser Glu Asp Ala Ser Leu Tyr Lys Leu Glu Asp Gly Ser
        115             120             125


Val Glu Gly Leu Ala Leu Thr Ile Phe Asp Lys Asn Lys Gly Ser Ile
    130             135             140


Ser Asn Asp Val Lys Ser Met Val Phe Ser Leu Thr Ser Ser Val Asp
145             150             155             160


Asn Ile Leu His Phe Phe Ala Ala Tyr Lys Ala Leu Lys Asn Asn Val
            165             170             175


Gln Pro Gly Asp Ala Asn Ala Ser Val Ser Phe Ile Val Thr Tyr Asp
            180             185             190
```

```
<210>    15
<211>    201
<212>    PRT
<213>    Escherichia coli
<400>    15
```

```
Met Ile Lys Phe Arg Leu Tyr Ile Pro Pro Val Ile Leu Gly Phe Val
1               5               10              15


Ile Val Pro Leu Leu Val Trp Pro Thr Val Ile Ala Leu Ala Val Leu
            20              25              30


Ile Phe Thr Leu Thr Phe Leu Ala Glu Ile Ile Phe Ser Phe Pro Leu
        35              40              45


Leu Val Val Arg Ile Ser Leu Gln Glu Leu Gln Leu Glu Leu Leu Val
    50              55              60


Val Tyr Ala Leu Phe Phe Ser Val Met Gly Gly Ile Gly Trp Gln Phe
65              70              75              80
```

Ser Arg Arg Thr Pro Pro Glu Leu Lys Asn Arg Leu His Cys Trp Leu
            85   90   95

Val Phe Ser Pro Val Tyr Phe Trp Leu Ile Leu Ser Asn Phe Ile Leu
            100   105   110

Tyr Ile Ser Pro Glu Lys Ser Ala Leu Leu Glu Asn Ile Arg Asn Phe
            115   120   125

Phe Leu Thr Phe Val Trp Leu Pro Leu Asn Phe Ser Pro Phe Trp Pro
            130   135   140

Gln Pro Trp Thr Asp Phe Val Gly Pro Ile Ser Ala Gln Leu Gly Phe
145   150   155   160

Ala Leu Gly Tyr Tyr Cys Gln Trp Arg Ser Lys Asn Arg Ser His Arg
                165   170   175

Lys Lys Trp Gly Asp Trp Val Thr Cys Leu Ser Leu Ala Ile Leu Ala
                180   185   190

Leu Gly Pro Leu Phe Asn Tyr Leu Gln
            195   200

<210>   16
<211>   234
<212>   PRT
<213>   Escherichia coli
<400>   16

Met Lys Phe Asn Leu Ser Asn Leu Ser Ala Val Leu Leu Ala Ser Gly
1   5   10   15

Met Leu Met Ser Thr Ala Val Thr Ala Ala Pro Gly Asp Ala Thr Gln
            20   25   30

Phe Gly Gly Ala Asp Thr Asp Trp Ser Thr Val Asp Tyr Pro Arg Leu
            35   40   45

Thr Asp Met Asp Asp Asn Val Asp Ser Met Gly Gly Lys Ile Arg Phe
        50   55   60

Thr Gly Arg Val Val Lys Ala Thr Cys Lys Val Ala Thr Asp Ser Lys

```
65                       70                      75                      80
```

Gln Ile Glu Val Val Leu Pro Val Val Pro Ser Asn Leu Phe Thr Gly
                    85   90   95

Ile Asp Val Glu Ala Gln Gly Ala Ser Asn Gln Thr Asp Phe Asn Ile
                    100   105   110

Asn Leu Thr Glu Cys Ser Asn Thr Asp Asp Gln Lys Ile Glu Phe Arg
            115   120   125

Phe Thr Gly Thr Ala Asp Ser Ala Asn Lys Thr Leu Ala Asn Glu Val
        130   135   140

Glu Gly Ser Thr Asp Ala Asp Asn Ser Gly Asn Ala Gly Ala Thr Gly
145   150   155   160

Val Gly Ile Arg Ile Tyr Ser Lys Gly Thr Thr Asn Asn Gly Leu Ile
                165   170   175

Asn Leu Asn Thr Thr Ala Ala Glu Gly Ser Ala Ser Thr Ala Ala Tyr
            180   185   190

Thr Ile Pro Gly Asn Ala Thr Thr His Asp Phe Ser Ala Ala Phe Thr
            195   200   205

Ala Gly Tyr Ala Gln Asn Gly Ser Thr Val Ala Pro Gly Val Val Lys
        210   215   220

Ser Thr Ala Ser Phe Val Val Leu Tyr Glu
225   230

```
<210>   17
<211>   336
<212>   PRT
<213>   Escherichia coli
<400>   17
```

Met Arg Ile His Thr Tyr Trp Tyr Arg Arg Tyr Phe Ile Leu Leu Ile
1   5   10   15

Ile Ile Phe Ser Asn Val Leu Ser Ser Ile Ala Asn Ala Glu Asp Met
                20   25   30

Gly Arg Glu Arg Ala Tyr Cys Tyr Pro Gly Ser Pro Ser Asn Asn Thr
        35   40   45

Thr Pro Ala Ser Phe Ser Tyr Asn Phe Gly Thr Ile Val Val Ser Asp
    50   55   60

Val Asn Lys Asn Ala Pro Gly Thr Val Leu Pro Ser Gln Ile Trp Lys
65   70   75   80

Val Gly Thr Tyr Lys Ala Tyr Cys Asn Ser Leu Asp Asp Tyr Glu Ile
                85   90   95

Tyr Phe Ser Ala Val Ser Gly Ile Asp Pro Ser Gly Ala Ser Gly Asp
            100   105   110

His Gln Gly Ser Asp Val Phe Ile Pro Leu Thr His Glu Ile Ser Val
        115   120   125

Ser Thr His Ile Lys Leu Tyr Asn Gln Asn Gly Thr Met Thr Asp Lys
    130   135   140

Ile Val Pro Phe Glu Asn Tyr Asn Thr Asn Tyr Pro Gly Asp Arg Ser
145   150   155   160

Lys Pro Ser Asn Trp Ala Ser Gly Thr Glu Gly Tyr Ile Lys Ile Arg
                165   170   175

Ile Asp Lys Lys Ile Ile Ser Asp Val Ser Leu Ser Asn Val Leu Leu
            180   185   190

Val Ser Leu Tyr Val Ser Gln Ile Pro Thr Glu His Gly Pro Ile Pro
        195   200   205

Val Phe Asn Ala Tyr Ile Gly Asn Leu Asn Ile Gln Val Pro Gln Gly
    210   215   220

Cys Thr Ile Asn Glu Gly Thr Ser Phe Thr Val Asn Met Pro Asp Val
225   230   235   240

Trp Ala Ser Glu Leu Ser Arg Ala Gly Ala Gly Ala Lys Pro Ala Gly
                245   250   255

Val Thr Pro Val Ala Thr Thr Ile Pro Ile Asn Cys Thr Asn Lys Asp

35

```
        260                    265                    270
```

Thr Asp Ala Val Met Thr Leu Val Phe Asp Gly Asn Ile Ser Ala Thr
        275   280   285

Arg Asp Thr Asn Gly Lys Gln Ser Ile Ile Gln Ala Gln Asp Asn Pro
        290   295   300

Asp Val Gly Ile Met Ile Met Asp Ser Gln Gln Asn Ser Val Asp Leu
305   310   315   320

Asn Ala Leu Ala Thr Ser Val Gly Val Pro Phe Arg Leu Val Glu Asn
                       325   330   335

```
<210>   18
<211>   864
<212>   PRT
<213>   Escherichia coli
<400>   18
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Met Asn Leu Lys Leu Lys Arg Cys Glu Tyr Trp Met Ala Ala Gln Lys
1   5   10   15

Gln Met Lys Arg Val Val Pro Leu Leu Leu Val Ile Met Pro Ala Cys
              20   25   30

Ser Ile Ala Gly Met Arg Phe Asn Pro Ala Phe Leu Ser Gly Asp Thr
              35   40   45

Glu Ala Val Ala Asp Leu Ser Arg Phe Glu Lys Gly Met Thr Tyr Leu
        50   55   60

Pro Gly Ser Tyr Glu Val Glu Val Trp Val Asn Asp Ser Pro Leu Leu
65   70   75   80

Ser Arg Thr Val Thr Phe Lys Ala Asp Asp Glu Asn Gln Leu Ile Pro
                  85   90   95

Cys Leu Ser Leu Ala Asp Leu Leu Ser Leu Gly Ile Asn Lys Asn Ala
              100   105   110

Leu Pro Glu Gln Ala Leu Ala Ser Ser Glu Asn Ser Cys Leu Asp Leu
        115   120   125

36

Arg Ile Trp Phe Pro Asp Val His Tyr Met Pro Glu Leu Asp Ala Gln
    130   135   140

Arg Leu Lys Leu Thr Phe Pro Gln Ala Ile Ile Lys Arg Asp Ala Arg
145   150   155   160

Gly Tyr Ile Pro Pro Glu Gln Trp Asp Asn Gly Ile Thr Ala Phe Leu
                 165   170   175

Leu Asn Tyr Asp Phe Ser Gly Asn Asn Asp Arg Gly Asp Tyr Ser Ser
            180   185   190

Asn Asn Tyr Tyr Leu Asn Leu Arg Ala Gly Ile Asn Ile Gly Ala Trp
        195   200   205

Arg Phe Arg Asp Tyr Ser Thr Trp Ser Arg Gly Ser Asn Ser Ala Gly
    210   215   220

Lys Leu Glu His Ile Ser Ser Thr Leu Gln Arg Val Ile Ile Pro Phe
225   230   235   240

Arg Ser Glu Leu Thr Leu Gly Asp Thr Trp Ser Ser Ser Asp Val Phe
                 245   250   255

Asp Ser Val Ser Ile Arg Gly Ile Lys Leu Glu Ser Asp Glu Asn Met
            260   265   270

Leu Pro Asp Ser Gln Ser Gly Phe Ala Pro Thr Val Arg Gly Ile Ala
        275   280   285

Lys Ser Arg Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Val Ile Tyr
290   295   300

Gln Thr Tyr Met Pro Pro Gly Pro Phe Glu Ile Ser Asp Leu Asn Pro
305   310   315   320

Thr Ser Ser Ala Gly Asp Leu Glu Val Thr Ile Lys Glu Ser Asp Asn
            325   330   335

Ser Glu Thr Val Tyr Thr Val Pro Tyr Ala Ala Val Pro Ile Leu Gln
            340   345   350

Arg Glu Gly His Leu Lys Tyr Ser Thr Thr Val Gly Gln Tyr Arg Ser

355   360   365

Asn Ser Tyr Asn Gln Lys Ser Pro Tyr Val Phe Gln Gly Glu Leu Ile
     370   375   380

Trp Gly Leu Pro Trp Asp Ile Thr Ala Tyr Gly Gly Ala Gln Phe Ser
385   390   395   400

Glu Asp Tyr Arg Ala Leu Ala Leu Gly Leu Gly Leu Asn Leu Gly Val
        405   410   415

Phe Gly Ala Thr Ser Phe Asp Val Thr Gln Ala Asn Ser Ser Leu Val
       420   425   430

Asp Gly Ser Lys His Gln Gly Gln Ser Tyr Arg Phe Leu Tyr Ser Lys
    435   440   445

Ser Leu Val Gln Thr Gly Thr Ala Phe His Ile Ile Gly Tyr Arg Tyr
 450   455   460

Ser Thr Gln Gly Phe Tyr Thr Leu Ser Asp Thr Thr Tyr Gln Gln Met
465   470   475   480

Ser Gly Thr Val Val Asp Pro Lys Thr Leu Asp Asp Lys Asp Tyr Val
       485   490   495

Tyr Asn Trp Asn Asp Phe Tyr Asn Leu Arg Tyr Ser Lys Arg Gly Lys
       500   505   510

Phe Gln Ala Ser Val Ser Gln Pro Phe Gly Asn Tyr Gly Ser Met Tyr
     515   520   525

Leu Ser Ala Ser Gln Gln Thr Tyr Trp Asn Thr Asp Lys Lys Asp Ser
   530   535   540

Leu Tyr Gln Val Gly Tyr Asn Thr Ser Ile Lys Gly Ile Tyr Leu Asn
545   550   555   560

Val Ala Trp Asn Tyr Ser Lys Ser Pro Gly Thr Asn Ala Asp Lys Ile
      565   570   575

Val Ser Leu Asn Val Ser Leu Pro Ile Ser Asn Trp Leu Ser Ser Thr
      580   585   590

```
Asn Asp Gly Arg Ser Ser Ser Asn Ala Met Thr Ala Thr Tyr Gly Tyr
        595             600             605

Ser Gln Asp Asn His Gly Gln Val Asn Gln Tyr Thr Gly Val Ser Gly
    610             615             620

Ser Leu Leu Glu Gln His Asn Leu Ser Tyr Asn Ile Gln His Gly Phe
625             630             635             640

Ala Asn Gln Asp Asn Ser Ser Ser Gly Ser Val Gly Val Asn Tyr Arg
            645             650             655

Gly Ala Tyr Gly Ser Leu Asn Ser Ala Tyr Ser Tyr Asp Asn Glu Gly
        660             665             670

Asn Gln Gln Ile Asn Tyr Gly Ile Ser Gly Ala Leu Val Val His Glu
    675             680             685

Asn Gly Leu Thr Leu Ser Gln Pro Leu Gly Glu Thr Asn Val Leu Ile
    690             695             700

Lys Ala Pro Gly Ala Asn Asn Val Asp Val Gln Arg Gly Thr Gly Ile
705             710             715             720

Ser Thr Asp Trp Arg Gly Tyr Ala Val Val Pro Tyr Ala Thr Glu Tyr
            725             730             735

Arg Arg Asn Asn Ile Ser Leu Asp Pro Met Ser Met Asn Met His Thr
            740             745             750

Glu Leu Asp Ile Thr Ser Thr Glu Val Ile Pro Gly Lys Gly Ala Leu
    755             760             765

Val Arg Ala Glu Phe Ala Ala His Ile Gly Ile Arg Gly Leu Phe Thr
    770             775             780

Val Arg Tyr Arg Asn Lys Ser Val Pro Phe Gly Ala Thr Ala Ser Ala
785             790             795             800

Gln Ile Lys Asn Ser Ser Gln Ile Thr Gly Ile Val Gly Asp Asn Gly
            805             810             815
```

```
Gln Leu Tyr Leu Ser Gly Leu Pro Leu Glu Gly Val Ile Asn Ile Gln
            820             825             830

Trp Gly Asp Gly Val Gln Gln Lys Cys Gln Ala Asn Tyr Lys Leu Pro
            835             840             845

Glu Thr Glu Leu Asp Asn Pro Val Ser Tyr Ala Thr Leu Glu Cys Arg
            850             855             860
```

<210> 19
<211> 169
<212> PRT
<213> Escherichia coli
<400> 19

```
Met Gly Ala Ile Tyr Val Lys Arg Leu Ile Leu Ser Val Ala Leu Ile
1               5               10              15

Ile Pro Ile Ala Ser Asn Ala Ser Asp Ala Leu Asn Gln Pro Ser Ser
            20              25              30

Ser Leu Asn Asp Gly Val Glu Thr Phe Phe Ile Ser Cys Phe Asp Met
            35              40              45

Pro Gln Glu Thr Thr Thr Asp Met Asp Ala Cys Gln Arg Val Gln Leu
            50              55              60

Ala Gln Val Ser Trp Val Lys Asn Lys Tyr Ser Val Ala Ala Leu Asn
65              70              75              80

Arg Leu Lys Gln Asp Asn Lys Asp Asp Pro Gln Arg Leu Gln Glu Leu
            85              90              95

Thr Ala Ser Phe Asn Ala Glu Ser Glu Ala Trp Thr Glu Leu Ile Glu
            100             105             110

Lys Ala Ser Lys Ser Val Gln Val Asp Tyr Val Gly Gly Thr Ile Ala
            115             120             125

Gly Thr Ala Val Ala Ser Arg Gln Ile Gly Leu Leu Glu Leu Gln Ser
            130             135             140

His Asp Ile Trp Glu His Trp Leu Arg Ser Arg Gly Leu Asn Ser Ser
145             150             155             160
```

```
Ser Phe Ala Arg Thr Lys Val Gln Ile
                165


<210>  20
<211>  713
<212>  PRT
<213>  Escherichia coli
<400>  20

Met Ala Met Phe Thr Pro Ser Phe Ser Gly Leu Lys Gly Arg Ala Leu
1               5                   10                  15


Phe Ser Leu Leu Phe Ala Ala Pro Met Ile His Ala Thr Asp Ser Val
                20                  25                  30


Thr Thr Lys Asp Gly Glu Thr Ile Thr Val Thr Ala Asp Ala Asn Thr
        35                  40                  45


Ala Thr Glu Ala Thr Asp Gly Tyr Gln Pro Leu Ser Thr Ser Thr Ala
    50                  55                  60


Thr Leu Thr Asp Met Pro Met Leu Asp Ile Pro Gln Val Val Asn Thr
65                  70                  75                  80


Val Ser Asp Gln Val Leu Glu Asn Gln Asn Ala Thr Thr Leu Asp Glu
                85                  90                  95


Ala Leu Tyr Asn Val Ser Asn Val Val Gln Thr Asn Thr Leu Gly Gly
                100                 105                 110


Thr Gln Asp Ala Phe Val Arg Arg Gly Phe Gly Ala Asn Arg Asp Gly
        115                 120                 125


Ser Ile Met Thr Asn Gly Leu Arg Thr Val Leu Pro Arg Ser Phe Asn
    130                 135                 140


Ala Ala Thr Glu Arg Val Glu Val Leu Lys Gly Pro Ala Ser Thr Leu
145                 150                 155                 160


Tyr Gly Ile Leu Asp Pro Gly Gly Leu Ile Asn Val Val Thr Lys Arg
                165                 170                 175


Pro Glu Lys Thr Phe His Gly Ser Val Ser Ala Thr Ser Ser Ser Phe
```

```
                  180                    185                    190
Gly Gly Gly Thr Gly Gln Leu Asp Ile Thr Gly Pro Ile Glu Gly Thr
           195                    200                    205

Gln Leu Ala Tyr Arg Leu Thr Gly Glu Val Gln Asp Glu Asp Tyr Trp
       210                    215                    220

Arg Asn Phe Gly Lys Glu Arg Ser Thr Phe Ile Ala Pro Ser Leu Thr
225                    230                    235                    240

Trp Phe Gly Asp Asn Ala Thr Val Thr Met Leu Tyr Ser His Arg Asp
               245                    250                    255

Tyr Lys Thr Pro Phe Asp Arg Gly Thr Ile Phe Asp Leu Thr Thr Lys
           260                    265                    270

Gln Pro Val Asn Val Asp Arg Lys Ile Arg Phe Asp Glu Pro Phe Asn
           275                    280                    285

Ile Thr Asp Gly Gln Ser Asp Leu Ala Gln Leu Asn Ala Glu Tyr His
       290                    295                    300

Leu Asn Ser Gln Trp Thr Ala Arg Phe Asp Tyr Ser Tyr Ser Gln Asp
305                    310                    315                    320

Lys Tyr Ser Asp Asn Gln Ala Arg Val Thr Ala Tyr Asp Ala Thr Thr
               325                    330                    335

Gly Thr Leu Thr Arg Arg Val Asp Ala Thr Gln Gly Ser Thr Gln Arg
               340                    345                    350

Met His Ala Thr Arg Ala Asp Leu Gln Gly Asn Val Asp Ile Ala Gly
           355                    360                    365

Phe Tyr Asn Glu Ile Leu Gly Gly Val Ser Tyr Glu Tyr Tyr Asp Leu
       370                    375                    380

Leu Arg Thr Asp Met Ile Arg Cys Lys Lys Ala Lys Asp Phe Asn Ile
385                    390                    395                    400

Tyr Asn Pro Val Tyr Gly Asn Thr Ser Lys Cys Thr Thr Val Ser Ala
               405                    410                    415
```

Ser Asp Ser Asp Gln Thr Ile Lys Gln Glu Asn Tyr Ser Ala Tyr Ala
            420   425   430

Gln Asp Ala Leu Tyr Leu Thr Asp Asn Trp Ile Ala Val Ala Gly Ile
            435   440   445

Arg Tyr Gln Tyr Tyr Thr Gln Tyr Ala Gly Lys Gly Arg Pro Phe Asn
    450   455   460

Val Asn Thr Asp Ser Arg Asp Glu Gln Trp Thr Pro Lys Leu Gly Leu
465   470   475   480

Val Tyr Lys Leu Thr Pro Ser Val Ser Leu Phe Ala Asn Tyr Ser Gln
            485   490   495

Thr Phe Met Pro Gln Ser Ser Ile Ala Ser Tyr Ile Gly Asp Leu Pro
            500   505   510

Pro Glu Ser Ser Asn Ala Tyr Glu Val Gly Ala Lys Phe Glu Leu Phe
            515   520   525

Asp Gly Ile Thr Ala Asp Ile Ala Leu Phe Asp Ile His Lys Arg Asn
    530   535   540

Val Leu Tyr Thr Glu Ser Ile Gly Asp Glu Thr Ile Ala Lys Thr Ala
545   550   555   560

Gly Arg Val Arg Ser Arg Gly Val Glu Val Asp Leu Ala Gly Ala Leu
            565   570   575

Thr Glu Asn Ile Asn Ile Ile Ala Ser Tyr Gly Tyr Thr Asp Ala Lys
            580   585   590

Val Leu Glu Asp Pro Asp Tyr Ala Gly Lys Pro Leu Pro Asn Val Pro
            595   600   605

Arg His Thr Gly Ser Leu Phe Leu Thr Tyr Asp Ile His Asn Met Pro
    610   615   620

Gly Asn Asn Thr Leu Thr Phe Gly Gly Gly Gly His Gly Val Ser Arg
625   630   635   640

Arg Ser Ala Thr Asn Gly Ala Asp Tyr Tyr Leu Pro Gly Tyr Phe Val
            645   650   655

Ala Asp Ala Phe Ala Ala Tyr Lys Met Lys Leu Gln Tyr Pro Val Thr
            660   665   670

Leu Gln Leu Asn Val Lys Asn Leu Phe Asp Lys Thr Tyr Tyr Thr Ser
        675   680   685

Ser Ile Ala Thr Asn Asn Leu Gly Asn Gln Ile Gly Asp Pro Arg Glu
     690   695   700

Val Gln Phe Thr Val Lys Met Glu Phe
705   710

<210> 21
<211> 606
<212> PRT
<213> Escherichia coli
<400> 21

Met Lys Ile Ser Trp Asn Tyr Ile Phe Lys Asn Lys Trp Arg Phe His
1   5   10   15

Ile Thr Ser Ile Ser Leu Phe Leu Ile Met Leu Ala Val Ser Ile Ala
           20   25   30

Phe Leu His Leu Arg Phe Asn Thr Leu Ser Ser Thr Asp Lys Met Arg
        35   40   45

Leu Glu Met Tyr Lys Ser Thr Leu Tyr Ser Thr Ile Glu Gln Phe Tyr
     50   55   60

Val Leu Pro Tyr Met Leu Ser Thr Asp His Ile Ile Arg Gln Ala Val
65   70   75   80

Ile Thr Pro Asp Asp Met Thr Ser Ser Glu Leu Asn Gln Arg Ile Ala
           85   90   95

His Phe Asn Thr Gln Leu Lys Thr Ala Ala Ile Phe Ile Leu Asp Thr
        100   105   110

Gln Gly Lys Ala Ile Ala Ser Ser Asn Trp Gln Asp Pro Gly Ser Tyr
      115   120   125

```
Val Gly Gln Asn Tyr Ser Tyr Arg Pro Tyr Tyr Lys His Ala Met Ser
    130             135             140

Gly Leu Asn Gly Arg Phe Tyr Gly Ile Gly Ser Thr Thr Asn Thr Pro
145             150             155             160

Gly Phe Phe Leu Ser Thr Ser Ile Lys Asp Lys Gly Lys Ile Val Gly
            165             170             175

Val Val Val Val Lys Ile Ser Leu Asn Glu Ile Glu Lys Ala Trp Ala
        180             185             190

Glu Gly Pro Glu Asn Ile Ile Val Asn Asp Glu His Gly Ile Ile Phe
            195             200             205

Leu Ser Ser Lys Ser Pro Trp Arg Met Arg Thr Leu Gln Pro Leu Pro
    210             215             220

Val Gln Ala Lys Gln Lys Leu Gln Ser Thr Arg Gln Tyr Ser Leu Asp
225             230             235             240

Asn Leu Leu Pro Ala Asp Tyr Tyr Pro Cys Tyr Thr Val Ser Asn Phe
            245             250             255

Thr Phe Leu Lys Asp Lys Lys Glu Gln Leu Cys Leu Phe Pro Gln Tyr
            260             265             270

Tyr Thr Gln Gln Ile Ala Ile Pro Glu Phe Asn Trp Lys Met Thr Ile
        275             280             285

Met Val Pro Leu Asp Asn Leu Tyr Trp Ser Trp Ala Ile Ser Leu Val
    290             295             300

Ile Thr Leu Ile Ile Tyr Leu Leu Phe Leu Leu Phe Ile Lys Tyr Trp
305             310             315             320

Arg Met Arg Ser His Ala Gln Gln Leu Leu Thr Leu Ala Asn Glu Thr
            325             330             335

Leu Glu Lys Gln Val Lys Glu Arg Thr Ser Ala Leu Glu Leu Ile Asn
        340             345             350
```

```
Gln Lys Leu Ile Gln Glu Ile Lys Glu Arg Ser Gln Ala Glu Gln Val
    355                 360                 365

Leu Gln Ile Thr Arg Ser Glu Leu Ala Glu Ser Ser Lys Leu Ala Ala
    370                 375                 380

Leu Gly Gln Met Ala Thr Glu Ile Ala His Glu Gln Asn Gln Pro Leu
385                 390                 395                 400

Ala Ala Ile His Ala Leu Thr Asp Asn Ala Arg Thr Met Leu Lys Lys
                405                 410                 415

Glu Met Tyr Pro Gln Val Glu Gln Asn Leu Lys His Ile Ile Ser Val
            420                 425                 430

Ile Glu Arg Met Thr Gln Leu Ile Ser Glu Leu Lys Ala Phe Ala Ser
    435                 440                 445

Arg His Arg Val Pro Lys Gly Ser Ala Asp Val Ile Lys Val Met Tyr
    450                 455                 460

Ser Ala Val Ala Leu Leu Asn His Ser Met Glu Lys Asn Asn Ile Glu
465                 470                 475                 480

Arg Arg Ile Lys Ala Pro Ser Met Pro Leu Phe Val Asn Cys Asp Glu
                485                 490                 495

Leu Gly Leu Glu Gln Ile Phe Ser Asn Leu Ile Ser Asn Ala Leu Asp
            500                 505                 510

Ser Met Glu Gly Ser Ser Tyr Lys Arg Leu Asp Ile Ala Ile Arg Gln
            515                 520                 525

Ala Asn Asn Lys Val Ile Ile Thr Ile Lys Asp Ser Gly Gly Gly Phe
    530                 535                 540

Ala Pro Glu Val Val Asp Arg Ile Phe Glu Pro Phe Phe Thr Thr Lys
545                 550                 555                 560

Arg Arg Gly Met Gly Leu Gly Leu Ala Ile Val Ser Glu Ile Val Arg
                565                 570                 575
```

Asn Ser Asn Gly Ala Leu His Ala Ser Asn His Pro Glu Gly Gly Ala
            580   585   590

Val Met Thr Leu Thr Trp Pro Glu Trp Gly Glu Glu His Glu
            595   600   605

<210> 22
<211> 101
<212> PRT
<213> Escherichia coli
<400> 22

Val Leu Thr Pro Gln His Leu Arg Cys Val Leu Thr Cys Ser Asp Leu
1   5   10   15

Leu Thr Leu Leu Ser Gly Thr Val Met Ser Gln Met Pro Leu Tyr Phe
            20   25   30

Leu Asn Thr Gln Lys Lys Leu Thr Ala His Tyr Glu Trp Leu Gln Ile
            35   40   45

Asn Leu Thr Asp Thr Tyr Glu Leu Val Lys Arg Leu Met Pro Ile Pro
    50   55   60

Ser Leu Asp Val Val Val Lys Val Gly Lys Leu Val Leu Pro Glu Lys
65   70   75   80

Gly His His Gly Phe Tyr Pro Glu Ala Gly Val Val Tyr Arg Thr Val
            85   90   95

Ala Pro Glu Asn Pro
            100

<210> 23
<211> 263
<212> PRT
<213> Escherichia coli
<400> 23

Met Met Lys Asn Thr Gly Tyr Ile Leu Ala Leu Cys Leu Thr Ala Ser
1   5   10   15

Gly His Val Leu Ala His Asp Val Trp Ile Thr Gly Lys Gln Ala Glu
            20   25   30

Asn Asn Val Thr Ala Glu Ile Gly Tyr Gly His Asn Phe Pro Ser Lys

```
            35                    40                    45

Gly Thr Ile Pro Asp Arg Arg Asp Phe Phe Glu Asn Pro Arg Leu Tyr
    50                  55                  60

Asn Gly Lys Glu Thr Ile Thr Leu Lys Pro Ala Ser Thr Asp Tyr Val
65                  70                  75                  80

Tyr Lys Thr Glu Ser Ala Ser Lys Asp Asn Gly Tyr Val Leu Ser Thr
                85                  90                  95

Tyr Met Lys Pro Gly Tyr Trp Ser Arg Thr Ser Ser Gly Trp Lys Pro
            100                 105                 110

Val Ser Arg Glu Gly Arg Asn Asp Val Ala Tyr Cys Glu Phe Val Thr
            115                 120                 125

Lys Tyr Ala Lys Ser Phe Ile Pro Gly Glu Gln Gln Met Pro Ala Gln
    130                 135                 140

Leu Tyr Gln Ser Pro Thr Gly His Glu Leu Glu Ile Ile Pro Leu Ser
145                 150                 155                 160

Asp Ile Ser Arg Phe Ser Glu Asn Val Lys Leu Lys Val Leu Tyr Lys
                165                 170                 175

Thr Ser Pro Leu Ala Gly Ala Ile Met Glu Leu Asp Ser Val Ser Tyr
            180                 185                 190

Leu Thr Ser Ser Arg His Thr His Ala Val Glu His Lys His Pro Val
            195                 200                 205

His Lys Ala Glu Leu Thr Phe Val Thr Asn Glu Asp Gly Ile Val Thr
    210                 215                 220

Val Pro Ser Leu His Ile Gly Gln Trp Leu Ala Lys Val Gln Asn Lys
225                 230                 235                 240

Lys Ser Phe Gln Asp Lys Ser Leu Cys Asp Glu Thr Val Asp Val Ala
                245                 250                 255

Thr Leu Ser Phe Ser Arg Asn
            260
```

```
<210>   24
<211>   378
<212>   PRT
<213>   Escherichia coli
<400>   24
```

Met Gly Lys Ile Lys Tyr Trp Leu Ile Val Gly Phe Ile Ile Leu Phe
1   5   10   15

Ala Ile Phe Tyr Ile Ala Ile Ser Asp Arg Asp Ser Thr Leu Ser Arg
            20   25   30

Leu Lys Ser Ala Gly Glu Asn Gly Asp Val Glu Ala Gln Tyr Ala Leu
        35   40   45

Gly Leu Met Tyr Leu Tyr Gly Glu Ile Leu Asp Val Asp Tyr Gln Gln
    50   55   60

Ala Lys Ile Trp Tyr Glu Lys Ala Ala Asp Gln Asn Asp Pro Arg Ala
65   70   75   80

Gln Ala Lys Leu Gly Val Met Tyr Ala Asn Gly Leu Gly Val Asn Gln
            85   90   95

Asp Tyr Gln Gln Ser Lys Leu Trp Tyr Glu Lys Ala Ala Ala Gln Asn
            100   105   110

Asp Val Asp Ala Gln Phe Leu Leu Gly Glu Met Tyr Asp Asp Gly Leu
        115   120   125

Gly Val Ser Gln Asp Tyr Gln His Ala Lys Met Trp Tyr Glu Lys Ala
    130   135   140

Ala Ala Gln Asn Asp Glu Arg Ala Gln Val Asn Leu Ala Val Leu Tyr
145   150   155   160

Ala Lys Gly Asn Gly Val Glu Gln Asp Tyr Arg Gln Ala Lys Ser Trp
            165   170   175

Tyr Glu Lys Ala Ala Ala Gln Asn Ser Pro Asp Ala Gln Phe Ala Leu
            180   185   190

Gly Ile Leu Tyr Ala Asn Ala Asn Gly Val Glu Gln Asp Tyr Gln Gln

```
        195                    200                    205

Ala Lys Asp Trp Tyr Glu Lys Ala Ala Glu Gln Asn Phe Ala Asn Ala
    210                215                220

Gln Phe Asn Leu Gly Met Leu Tyr Tyr Lys Gly Glu Gly Val Lys Gln
225                230                235                240

Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn
            245                250                255

Gln Pro Asn Ala Gln Tyr Asn Leu Gly Gln Ile Tyr Tyr Tyr Gly Gln
                260                265                270

Gly Val Thr Gln Ser Tyr Arg Gln Ala Lys Asp Trp Phe Glu Lys Ala
        275                280                285

Ala Glu Lys Gly His Val Asp Ala Gln Tyr Asn Leu Gly Val Ile Tyr
    290                295                300

Glu Asn Gly Glu Gly Val Ser Gln Asn Tyr Gln Gln Ala Lys Ala Trp
305                310                315                320

Tyr Glu Lys Ala Ala Ser Gln Asn Asp Ala Gln Ala Gln Phe Glu Leu
            325                330                335

Gly Val Met Asn Glu Leu Gly Gln Gly Glu Ser Ile Asp Leu Lys Gln
            340                345                350

Ala Arg His Tyr Tyr Glu Arg Ser Cys Asn Asn Gly Leu Lys Lys Gly
        355                360                365

Cys Glu Arg Leu Lys Glu Leu Leu Tyr Lys
    370                375
```

<210> 25
<211> 654
<212> PRT
<213> Escherichia coli
<400> 25

```
Met Asn Val Ile Arg Thr Val Ile Cys Thr Leu Ile Ile Leu Pro Val
1               5               10                  15
```

```
Gly Leu Gln Ala Ala Thr Ser His Ser Ser Met Val Lys Asp Thr Ile
        20              25              30

Thr Ile Val Ala Thr Gly Asn Gln Asn Thr Val Phe Glu Thr Pro Ser
        35              40              45

Met Val Ser Val Val Thr Asn Asp Thr Pro Trp Ser Gln Asn Ala Val
    50              55              60

Thr Ser Ala Gly Met Leu Lys Gly Val Ala Gly Leu Ser Gln Thr Gly
65              70              75              80

Ala Gly Arg Thr Asn Gly Gln Thr Phe Asn Leu Arg Gly Tyr Asp Lys
            85              90              95

Ser Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Leu Ser Asp Met
        100             105             110

Ala Lys Ser Ser Gly Thr Tyr Leu Asp Pro Ala Leu Val Lys Arg Ile
        115             120             125

Glu Val Val Arg Gly Pro Asn Ser Ser Leu Tyr Gly Ser Gly Gly Leu
    130             135             140

Gly Gly Val Val Asp Phe Arg Thr Ala Asp Ala Ala Asp Phe Leu Pro
145             150             155             160

Pro Gly Glu Thr Asn Gly Leu Ser Leu Trp Gly Asn Ile Ala Ser Gly
            165             170             175

Asp His Ser Thr Gly Ser Gly Leu Thr Trp Phe Gly Lys Thr Gly Lys
        180             185             190

Thr Asp Ala Leu Leu Ser Val Ile Met Arg Lys Arg Gly Asn Ile Tyr
        195             200             205

Gln Ser Asp Gly Glu His Ala Pro Asn Lys Glu Lys Pro Ala Ala Leu
    210             215             220

Phe Ala Lys Gly Ser Val Gly Ile Thr Asp Ser Asn Lys Ala Gly Ala
225             230             235             240

Ser Leu Arg Leu Tyr Arg Asn Asn Thr Thr Glu Pro Gly Asn Ser Thr
```

                    245   250   255

    Gln Thr His Gly Asp Ser Gly Leu Arg Asp Arg Lys Thr Val Gln Asn
                  260   265   270

    Asp Val Gln Phe Trp Tyr Gln Tyr Ala Pro Val Asp Asn Ser Leu Ile
                  275   280   285

    Asn Val Lys Ser Thr Leu Tyr Leu Ser Asp Ile Thr Ile Lys Thr Asn
                  290   295   300

    Gly His Asn Lys Thr Ala Glu Trp Arg Asn Asn Arg Thr Ser Gly Val
    305   310   315   320

    Asn Val Val Asn Arg Ser His Thr Leu Ile Phe Pro Gly Ala His Gln
                  325   330   335

    Leu Ser Tyr Gly Ala Glu Tyr Tyr Arg Gln Gln Gln Lys Pro Glu Gly
                  340   345   350

    Ser Ala Thr Leu Tyr Pro Glu Gly Asn Ile Asp Phe Thr Ser Leu Tyr
                  355   360   365

    Phe Gln Asp Glu Met Thr Met Lys Ser Tyr Pro Val Asn Ile Ile Val
                  370   375   380

    Gly Ser Arg Tyr Asp Arg Tyr Lys Ser Phe Asn Pro Arg Ala Gly Glu
    385   390   395   400

    Leu Lys Ala Glu Arg Leu Ser Pro Arg Ala Ala Ile Ser Val Ser Pro
                  405   410   415

    Thr Asp Trp Leu Met Met Tyr Gly Ser Ile Ser Ser Ala Phe Arg Ala
                  420   425   430

    Pro Thr Met Ala Glu Met Tyr Arg Asp Asp Val His Phe Tyr Arg Lys
                  435   440   445

    Gly Lys Pro Asn Tyr Trp Val Pro Asn Leu Asn Leu Lys Pro Glu Asn
         450   455   460

    Asn Ile Thr Arg Glu Ile Gly Ala Gly Ile Gln Leu Asp Gly Leu Leu
    465   470   475   480

```
Thr Asp Asn Asp Arg Leu Gln Leu Lys Gly Gly Tyr Phe Gly Thr Asp
            485             490             495

Ala Arg Asn Tyr Ile Ala Thr Arg Val Asp Met Lys Arg Met Arg Ser
            500             505             510

Tyr Ser Tyr Asn Val Ser Arg Ala Arg Ile Trp Gly Trp Asp Met Gln
            515             520             525

Gly Asn Tyr Gln Ser Asp Tyr Val Asp Trp Met Leu Ser Tyr Asn Arg
    530             535             540

Thr Glu Ser Met Asp Ala Ser Ser Arg Glu Trp Leu Gly Ser Gly Asn
545             550             555             560

Pro Asp Thr Leu Ile Ser Asp Ile Ser Ile Pro Val Gly His Arg Gly
            565             570             575

Val Tyr Ala Gly Trp Arg Ala Glu Leu Ser Ala Ser Ala Thr His Val
            580             585             590

Lys Lys Gly Asp Pro His Gln Ala Gly Tyr Thr Ile His Ser Phe Ser
    595             600             605

Leu Ser Tyr Lys Pro Val Ser Val Lys Gly Phe Glu Ala Ser Val Thr
    610             615             620

Leu Asp Asn Ala Phe Asn Lys Leu Ala Met Asn Gly Lys Gly Val Pro
625             630             635             640

Leu Ser Gly Arg Thr Val Ser Leu Tyr Thr Arg Tyr Gln Trp
            645             650
```

```
<210>  26
<211>  1376
<212>  PRT
<213>  Escherichia coli
<400>  26
```

```
Met Asn Lys Ile Tyr Ala Leu Lys Tyr Cys Tyr Ile Thr Asn Thr Val
1           5               10              15

Lys Val Val Ser Glu Leu Ala Arg Arg Val Cys Lys Gly Ser Thr Arg
```

53

```
                20                     25                    30

    Arg Gly Lys Arg Leu Ser Val Leu Thr Ser Leu Ala Leu Ser Ala Leu
            35                    40                    45

    Leu Pro Thr Val Ala Gly Ala Ser Thr Val Gly Gly Asn Asn Pro Tyr
        50                    55                    60

    Gln Thr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Gln Phe Gln Ala Gly
    65                    70                    75                    80

    Ala Thr Asn Ile Pro Ile Phe Asn Asn Lys Gly Glu Leu Val Gly His
                    85                    90                    95

    Leu Asp Lys Ala Pro Met Val Asp Phe Ser Ser Val Asn Val Ser Ser
                100                    105                    110

    Asn Pro Gly Val Ala Thr Leu Ile Asn Pro Gln Tyr Ile Ala Ser Val
                115                    120                    125

    Lys His Asn Lys Gly Tyr Gln Ser Val Ser Phe Gly Asp Gly Gln Asn
        130                    135                    140

    Ser Tyr His Ile Val Asp Arg Asn Glu His Ser Ser Ser Asp Leu His
    145                    150                    155                    160

    Thr Pro Arg Leu Asp Lys Leu Val Thr Glu Val Ala Pro Ala Thr Val
                165                    170                    175

    Thr Ser Ser Ser Thr Ala Asp Ile Leu Asn Pro Ser Lys Tyr Ser Ala
                180                    185                    190

    Phe Tyr Arg Ala Gly Ser Gly Ser Gln Tyr Ile Gln Asp Ser Gln Gly
            195                    200                    205

    Lys Arg His Trp Val Thr Gly Gly Tyr Gly Tyr Leu Thr Gly Gly Ile
        210                    215                    220

    Leu Pro Thr Ser Phe Phe Tyr His Gly Ser Asp Gly Ile Gln Leu Tyr
    225                    230                    235                    240

    Met Gly Gly Asn Ile His Asp His Ser Ile Leu Pro Ser Phe Gly Glu
                    245                    250                    255
```

Ala Gly Asp Ser Gly Ser Pro Leu Phe Gly Trp Asn Thr Ala Lys Gly
            260   265   270

Gln Trp Glu Leu Val Gly Val Tyr Ser Gly Val Gly Gly Gly Thr Asn
            275   280   285

Leu Ile Tyr Ser Leu Ile Pro Gln Ser Phe Leu Ser Gln Ile Tyr Ser
    290   295   300

Glu Asp Asn Asp Ala Pro Val Phe Phe Asn Ala Ser Ser Gly Ala Pro
305   310   315   320

Leu Gln Trp Lys Phe Asp Ser Ser Thr Gly Thr Gly Ser Leu Lys Gln
                325   330   335

Gly Ser Asp Glu Tyr Ala Met His Gly Gln Lys Gly Ser Asp Leu Asn
            340   345   350

Ala Gly Lys Asn Leu Thr Phe Leu Gly His Asn Gly Gln Ile Asp Leu
        355   360   365

Glu Asn Ser Val Thr Gln Gly Ala Gly Ser Leu Thr Phe Thr Asp Asp
    370   375   380

Tyr Thr Val Thr Thr Ser Asn Gly Ser Thr Trp Thr Gly Ala Gly Ile
385   390   395   400

Ile Val Asp Lys Asp Ala Ser Val Asn Trp Gln Val Asn Gly Val Lys
            405   410   415

Gly Asp Asn Leu His Lys Ile Gly Glu Gly Thr Leu Val Val Gln Gly
            420   425   430

Thr Gly Val Asn Glu Gly Gly Leu Lys Val Gly Asp Gly Thr Val Val
        435   440   445

Leu Asn Gln Gln Ala Asp Ser Ser Gly His Val Gln Ala Phe Ser Ser
    450   455   460

Val Asn Ile Ala Ser Gly Arg Pro Thr Val Val Leu Ala Asp Asn Gln
465   470   475   480

Gln Val Asn Pro Asp Asn Ile Ser Trp Gly Tyr Arg Gly Gly Val Leu
                485   490   495

Asp Val Asn Gly Asn Asp Leu Thr Phe His Lys Leu Asn Ala Ala Asp
            500   505   510

Tyr Gly Ala Thr Leu Gly Asn Ser Ser Asp Lys Thr Ala Asn Ile Thr
        515   520   525

Leu Asp Tyr Gln Thr Arg Pro Ala Asp Val Lys Val Asn Glu Trp Ser
    530   535   540

Ser Ser Asn Arg Gly Thr Val Gly Ser Leu Tyr Ile Tyr Asn Asn Pro
545   550   555   560

Tyr Thr His Thr Val Asp Tyr Phe Ile Leu Lys Thr Ser Ser Tyr Gly
            565   570   575

Trp Phe Pro Thr Gly Gln Val Ser Asn Glu His Trp Glu Tyr Val Gly
        580   585   590

His Asp Gln Asn Ser Ala Gln Ala Leu Leu Ala Asn Arg Ile Asn Asn
    595   600   605

Lys Gly Tyr Leu Tyr His Gly Lys Leu Leu Gly Asn Ile Asn Phe Ser
610   615   620

Asn Lys Ala Thr Pro Gly Thr Thr Gly Ala Leu Val Met Asp Gly Ser
625   630   635   640

Ala Asn Met Ser Gly Thr Phe Thr Gln Glu Asn Gly Arg Leu Thr Ile
            645   650   655

Gln Gly His Pro Val Ile His Ala Ser Thr Ser Gln Ser Ile Ala Asn
            660   665   670

Thr Val Ser Ser Leu Gly Asp Asn Ser Val Leu Thr Gln Pro Thr Ser
            675   680   685

Phe Thr Gln Asp Asp Trp Glu Asn Arg Thr Phe Ser Phe Gly Ser Leu
    690   695   700

Val Leu Lys Asp Thr Asp Phe Gly Leu Gly Arg Asn Ala Thr Leu Asn
705   710   715   720

Thr Thr Ile Gln Ala Asp Asn Ser Ser Val Thr Leu Gly Asp Ser Arg
              725   730   735

Val Phe Ile Asp Lys Lys Asp Gly Gln Gly Thr Ala Phe Thr Leu Glu
              740   745   750

Glu Gly Thr Ser Val Ala Thr Lys Asp Ala Asp Lys Ser Val Phe Asn
          755   760   765

Gly Thr Val Asn Leu Asp Asn Gln Ser Val Leu Asn Ile Asn Glu Ile
    770   775   780

Phe Asn Gly Gly Ile Gln Ala Asn Asn Ser Thr Val Asn Ile Ser Ser
785   790   795   800

Asp Ser Ala Val Leu Glu Asn Ser Thr Leu Thr Ser Thr Ala Leu Asn
              805   :   810   815

Leu Asn Lys Gly Ala Asn Val Leu Ala Ser Gln Ser Phe Val Ser Asp
          820   825   830

Gly Pro Val Asn Ile Ser Asp Ala Thr Leu Ser Leu Asn Ser Arg Pro
      835   840   845

Asp Glu Val Ser His Thr Leu Leu Pro Val Tyr Asp Tyr Ala Gly Ser
  . 850   855   860

Trp Asn Leu Lys Gly Asp Asp Ala Arg Leu Asn Val Gly Pro Tyr Ser
865   870   875   880

Met Leu Ser Gly Asn Ile Asn Val Gln Asp Lys Gly Thr Val Thr Leu
              885   890   895

Gly Gly Glu Gly Glu Leu Ser Pro Asp Leu Thr Leu Gln Asn Gln Met
          900   905   910

Leu Tyr Ser Leu Phe Asn Gly Tyr Arg Asn Thr Trp Ser Gly Ser Leu
          915   920   925

Asn Ala Pro Asp Ala Thr Val Ser Met Thr Asp Thr Gln Trp Ser Met

```
        930                    935                    940

Asn Gly Asn Ser Thr Ala Gly Asn Met Lys Leu Asn Arg Thr Ile Val
945                    950                    955                    960

Gly Phe Asn Gly Gly Thr Ser Ser Phe Thr Thr Leu Thr Thr Asp Asn
                       965                    970                    975

Leu Asp Ala Val Gln Ser Ala Phe Val Met Arg Thr Asp Leu Asn Lys
                  980                    985                    990

Ala Asp Lys Leu Val Ile Asn Lys  Ser Ala Thr Gly His  Asp Asn Ser
             995                    1000                    1005

Ile Trp  Val Asn Phe Leu Lys  Lys Pro Ser Asp Lys  Asp Thr Leu
     1010                    1015                    1020

Asp Ile  Pro Leu Val Ser Ala  Pro Glu Ala Thr Ala  Asp Asn Leu
     1025                    1030                    1035

Phe Arg  Ala Ser Thr Arg Val  Val Gly Phe Ser Asp  Val Thr Pro
     1040                    1045                    1050

Thr Leu  Ser Val Arg Lys Glu  Asp Gly Lys Lys Glu  Trp Val Leu
     1055                    1060                    1065

Asp Gly  Tyr Gln Val Ala Arg  Asn Asp Gly Gln Gly  Lys Ala Ala
     1070                    1075                    1080

Ala Thr  Phe Met His Ile Ser  Tyr Asn Asn Phe Ile  Thr Glu Val
     1085                    1090                    1095

Asn Asn  Leu Asn Lys Arg Met  Gly Asp Leu Arg Asp  Ile Asn Gly
     1100                    1105                    1110

Glu Ala  Gly Thr Trp Val Arg  Leu Leu Asn Gly Ser  Gly Ser Ala
     1115                    1120                    1125

Asp Gly  Gly Phe Thr Asp His  Tyr Thr Leu Leu Gln  Met Gly Ala
     1130                    1135                    1140

Asp Arg  Lys His Glu Leu Gly  Ser Met Asp Leu Phe  Thr Gly Val
     1145                    1150                    1155
```

```
Met Ala  Thr Tyr Thr Asp Thr  Asp Ala Ser Ala Gly  Leu Tyr Ser
    1160                 1165               1170

Gly Lys  Thr Lys Ser Trp Gly  Gly Gly Phe Tyr Ala  Ser Gly Leu
    1175                 1180               1185

Phe Arg  Ser Gly Ala Tyr Phe  Asp Leu Ile Ala Lys  Tyr Ile His
    1190                 1195               1200

Asn Glu  Asn Lys Tyr Asp Leu  Asn Phe Ala Gly Ala  Gly Lys Gln
    1205                 1210               1215

Asn Phe  Arg Ser His Ser Leu  Tyr Ala Gly Ala Glu  Val Gly Tyr
    1220                 1225               1230

Arg Tyr  His Leu Thr Asp Thr  Thr Phe Val Glu Pro  Gln Ala Glu
    1235                 1240               1245

Leu Val  Trp Gly Arg Leu Gln  Gly Gln Thr Phe Asn  Trp Asn Asp
    1250                 1255               1260

Ser Gly  Met Asp Val Ser Met  Arg Arg Asn Ser Val  Asn Pro Leu
    1265                 1270               1275

Val Gly  Arg Thr Gly Val Val  Ser Gly Lys Thr Phe  Ser Gly Lys
    1280                 1285               1290

Asp Trp  Ser Leu Thr Ala Arg  Ala Gly Leu His Tyr  Glu Phe Asp
    1295                 1300               1305

Leu Thr  Asp Ser Ala Asp Val  His Leu Lys Asp Ala  Ala Gly Glu
    1310                 1315               1320

His Gln  Ile Asn Gly Arg Lys  Asp Gly Arg Met Leu  Tyr Gly Val
    1325                 1330               1335

Gly Leu  Asn Ala Arg Phe Gly  Asp Asn Thr Arg Leu  Gly Leu Glu
    1340                 1345               1350

Val Glu  Arg Ser Ala Phe Gly  Lys Tyr Asn Thr Asp  Asp Ala Ile
    1355                 1360               1365
```

```
Asn Ala  Asn Ile Arg Tyr Ser  Phe
    1370                1375


<210>  27
<211>  349
<212>  PRT
<213>  Escherichia coli
<400>  27

Met Ile Thr Leu Phe Arg Leu Leu Ala Ile Leu Cys Leu Phe Phe Asn
1               5                  10                  15

Val Ser Ala Phe Ala Val Asp Cys Tyr Gln Asp Gly Tyr Arg Gly Thr
            20                  25                  30

Thr Leu Ile Asn Gly Asp Leu Pro Thr Phe Lys Ile Pro Glu Asn Ala
        35                  40                  45

Gln Pro Gly Gln Lys Ile Trp Glu Ser Gly Asp Ile Asn Ile Thr Val
    50                  55                  60

Tyr Cys Asp Asn Ala Pro Gly Trp Ser Ser Asn Asn Pro Ser Glu Asn
65                  70                  75                  80

Val Tyr Ala Trp Ile Lys Leu Pro Gln Ile Asn Ser Ala Asp Met Leu
                85                  90                  95

Asn Asn Pro Tyr Leu Thr Phe Gly Val Thr Tyr Asn Gly Val Asp Tyr
            100                 105                 110

Glu Gly Thr Asn Glu Lys Ile Asp Thr His Ala Cys Leu Asp Lys Tyr
        115                 120                 125

Glu Gln Tyr Tyr Asn Gly Tyr Tyr His Asp Pro Val Cys Asn Gly Ser
    130                 135                 140

Thr Leu Gln Lys Asn Val Thr Phe Asn Ala His Phe Arg Val Tyr Val
145                 150                 155                 160

Lys Phe Lys Ser Arg Pro Ala Gly Asp Gln Thr Val Asn Phe Gly Thr
            165                 170                 175

Val Asn Val Leu Gln Phe Asp Gly Glu Gly Gly Ala Asn Met Ala Pro
        180                 185                 190
```

```
Asn Ala Lys Asn Leu Arg Tyr Ala Ile Thr Gly Leu Asp Asn Ile Ser
        195                 200                 205

Phe Leu Asp Cys Ser Val Asp Val Arg Ile Ser Pro Glu Ser Gln Ile
        210                 215                 220

Val Asn Phe Gly Gln Ile Ala Ala Asn Ser Ile Ala Thr Phe Pro Pro
225                 230                 235                 240

Lys Ala Ala Phe Ser Val Ser Thr Ile Lys Asp Ile Ala Ser Asp Cys
                245                 250                 255

Thr Glu Gln Phe Asp Val Ala Thr Ser Phe Phe Thr Ser Asp Thr Leu
                260                 265                 270

Tyr Asp Asn Thr His Leu Glu Ile Gly Asn Gly Leu Leu Met Arg Ile
        275                 280                 285

Thr Asp Gln Lys Thr Gln Glu Asp Ile Lys Phe Asn Gln Phe Lys Leu
    290                 295                 300

Phe Ser Thr Tyr Ile Pro Gly Gln Ser Ala Ala Met Ala Thr Arg Asp
305                 310                 315                 320

Tyr Gln Ala Glu Leu Thr Gln Lys Pro Gly Glu Pro Leu Val Tyr Gly
                325                 330                 335

Pro Phe Gln Lys Asp Leu Ile Val Lys Ile Asn Tyr His
                340                 345
```

<210> 28
<211> 840
<212> PRT
<213> Escherichia coli
<400> 28

```
Met Asn Asn Lys Asn Thr Phe Ser Arg Asp Lys Leu Ser His Ala Ile
1               5                   10                  15

Lys Asn Ala Leu Ser Gly Val Val Cys Ser Leu Leu Phe Val Leu Pro
                20                  25                  30

Val His Ala Val Glu Phe Asn Val Asp Met Ile Asp Ala Glu Asp Arg
```

```
          35                    40                    45

Glu Asn Ile Asp Ile Ser Arg Phe Glu Lys Lys Gly Tyr Ile Pro Pro
    50                  55                  60


Gly Arg Tyr Leu Val Arg Val Gln Ile Asn Lys Asn Met Leu Pro Gln
65                  70                  75                  80


Thr Leu Ile Leu Glu Trp Val Lys Ala Asp Asn Glu Ser Gly Ser Leu
            85                  90                  95


Leu Cys Leu Thr Lys Glu Asn Leu Thr Asn Phe Gly Leu Asn Thr Glu
            100                 105                 110


Phe Ile Glu Ser Leu Gln Asn Ile Ala Gly Ser Glu Cys Leu Asp Leu
        115                 120                 125


Ser Gln Arg Gln Glu Leu Thr Thr Arg Leu Asp Lys Ala Thr Met Ile
    130                 135                 140


Leu Ser Leu Ser Val Pro Gln Ala Trp Leu Lys Tyr Gln Ala Thr Asn
145                 150                 155                 160


Trp Thr Pro Pro Glu Phe Trp Asp Thr Gly Ile Thr Gly Phe Ile Leu
            165                 170                 175


Asp Tyr Asn Val Tyr Ala Ser Gln Tyr Ala Pro His His Gly Asp Ser
            180                 185                 190


Thr Gln Asn Val Ser Ser Tyr Gly Thr Leu Gly Phe Asn Leu Gly Ala
        195                 200                 205


Trp Arg Leu Arg Ser Asp Tyr Gln Tyr Asn Gln Asn Phe Ala Asp Gly
    210                 215                 220


Arg Ser Val Asn Arg Asp Ser Glu Phe Ala Arg Thr Tyr Leu Phe Arg
225                 230                 235                 240


Pro Ile Pro Ser Trp Ser Ser Lys Phe Thr Met Gly Gln Tyr Asp Leu
            245                 250                 255


Ser Ser Asn Leu Tyr Asp Thr Phe His Phe Thr Gly Ala Ser Leu Glu
        260                 265                 270
```

```
Ser Asp Glu Ser Met Leu Pro Pro Asp Leu Gln Gly Tyr Ala Pro Gln
        275             280             285

Ile Thr Gly Ile Ala Gln Thr Asn Ala Lys Val Thr Val Ala Gln Asn
    290             295             300

Gly Arg Val Leu Tyr Gln Thr Thr Val Ala Pro Gly Pro Phe Thr Ile
305             310             315             320

Ser Asp Leu Gly Gln Ser Phe Gln Gly Gln Leu Asp Val Thr Val Glu
            325             330             335

Glu Glu Asp Gly Arg Thr Ser Thr Phe Gln Val Gly Ser Ala Ser Ile
            340             345             350

Pro Tyr Leu Thr Arg Lys Gly Gln Val Arg Tyr Lys Thr Ser Leu Gly
        355             360             365

Lys Pro Thr Ser Val Gly His Asn Asp Ile Asn Asn Pro Phe Phe Trp
    370             375             380

Thr Ala Glu Ala Ser Trp Gly Trp Leu Asn Asn Val Ser Leu Tyr Gly
385             390             395             400

Gly Gly Met Phe Thr Ala Asp Asp Tyr Gln Ala Ile Thr Thr Gly Ile
            405             410             415

Gly Phe Asn Leu Asn Gln Phe Gly Ser Leu Ser Phe Asp Val Thr Gly
        420             425             430

Ala Asp Ala Ser Leu Gln Gln Gln Asn Ser Gly Asn Leu Arg Gly Tyr
        435             440             445

Ser Tyr Arg Phe Asn Tyr Ala Lys His Phe Glu Ser Thr Gly Ser Gln
    450             455             460

Ile Thr Phe Ala Gly Tyr Arg Phe Ser Asp Lys Asp Tyr Val Ser Met
465             470             475             480

Ser Glu Tyr Leu Ser Ser Arg Asn Gly Asp Glu Ser Ile Asp Asn Glu
            485             490             495
```

Lys Glu Ser Tyr Val Ile Ser Leu Asn Gln Tyr Phe Glu Thr Leu Glu
            500   505   510

Leu Asn Ser Tyr Leu Asn Val Thr Arg Asn Thr Tyr Trp Asp Ser Ala
            515   520   525

Ser Asn Thr Asn Tyr Ser Val Ser Val Ser Lys Asn Phe Asp Ile Gly
    530   535   540

Asp Phe Lys Gly Ile Ser Ala Ser Leu Ala Val Ser Arg Ile Arg Trp
545   550   555   560

Asp Asp Asp Glu Glu Asn Gln Tyr Tyr Phe Ser Phe Ser Leu Pro Leu
                565   570   575

Gln Gln Asn Arg Asn Ile Ser Tyr Ser Met Gln Arg Thr Gly Ser Ser
            580   585   590

Asn Thr Ser Gln Met Ile Ser Trp Tyr Asp Ser Ser Asp Arg Asn Asn
        595   600   605

Ile Trp Asn Ile Ser Ala Ser Ala Thr Asp Asp Asn Ile Arg Asp Gly
    610   615   620

Glu Pro Thr Leu Arg Gly Ser Tyr Gln His Tyr Ser Pro Trp Gly Arg
625   630   635   640

Leu Asn Ile Asn Gly Ser Val Gln Pro Asn Gln Tyr Asn Ser Val Thr
                645   650   655

Ala Gly Trp Tyr Gly Ser Leu Thr Ala Thr Arg His Gly Val Ala Leu
            660   665   670

His Asp Tyr Ser Tyr Gly Asp Asn Ala Arg Met Met Val Asp Thr Asp
    675   680   685

Gly Ile Ser Gly Ile Glu Ile Asn Ser Asn Arg Thr Val Thr Asn Gly
    690   695   700

Leu Gly Ile Ala Val Ile Pro Ser Leu Ser Asn Tyr Thr Thr Ser Met
705   710   715   720

Leu Arg Val Asn Asn Asn Asp Leu Pro Glu Gly Val Asp Val Glu Asn
                725   730   735

Ser Val Ile Arg Thr Thr Leu Thr Gln Gly Ala Ile Gly Tyr Ala Lys
            740   745   750

Leu Asn Ala Thr Thr Gly Tyr Gln Ile Val Gly Val Ile Arg Gln Glu
            755   760   765

Asn Gly Arg Phe Pro Pro Leu Gly Val Asn Val Thr Asp Lys Ala Thr
        770   775   780

Gly Lys Asp Val Gly Leu Val Ala Glu Asp Gly Phe Val Tyr Leu Ser
785   790   795   800

Gly Ile Gln Glu Asn Ser Ile Leu His Leu Thr Trp Gly Asp Asn Thr
                805   810   815

Cys Glu Val Thr Pro Pro Asn Gln Ser Asn Ile Ser Glu Ser Ala Ile
                820   825   830

Ile Leu Pro Cys Lys Thr Val Lys
            835   840

<210> 29
<211> 169
<212> PRT
<213> Escherichia coli
<400> 29

Leu Met Asn Thr Lys Gln Ser Val Ala Gln Leu Ala Val Pro His Arg
1   5   10   15

Lys Arg Leu Ser Ser Thr Met Val Val Ala Leu Leu Leu Cys Val Val
            20   25   30

Ala Gly Ala Val Met Ile Asn Ala Ala Asp Phe Pro Ala Thr Ala Ile
        35   40   45

Glu Thr Asp Pro Gly Ala Ser Ala Phe Pro Thr Phe Tyr Ala Cys Ala
    50   55   60

Leu Ile Val Leu Ala Val Leu Leu Val Ile Arg Asp Leu Leu Gln Ala
65   70   75   80

Lys Pro Ala Ser Cys Ala Asn Ala Gln Glu Lys Pro Ala Phe Arg Lys
                85   90   95

Thr Ala Thr Gly Ile Ala Ala Thr Ala Phe Tyr Ile Val Ala Met Ser
            100   105   110

Tyr Cys Gly Tyr Leu Ile Thr Thr Pro Val Phe Leu Ile Val Ile Met
        115   120   125

Thr Leu Met Gly Tyr Arg Arg Trp Val Leu Thr Pro Gly Ile Ala Leu
    130   135   140

Leu Leu Thr Ala Ile Leu Trp Leu Leu Phe Val Glu Ala Leu Gln Val
145   150   155   160

Pro Leu Pro Val Gly Thr Phe Phe Glu
                165

<210> 30
<211> 311
<212> PRT
<213> Escherichia coli
<400> 30

Met Val Leu Leu Ala Gly Ala Ala Leu Ser Ile Ala Pro Val Gln Ala
1   5   10   15

Ala Ser Tyr Pro Thr Lys Gln Ile Glu Leu Val Val Pro Tyr Ala Ala
            20   25   30

Gly Gly Gly Thr Asp Leu Val Ala Arg Ala Phe Ala Asp Ala Ala Lys
            35   40   45

Asn His Leu Pro Val Ser Ile Gly Val Ile Asn Lys Pro Gly Gly Gly
    50   55   60

Gly Ala Ile Gly Leu Ser Glu Ile Ala Ala Ala Arg Pro Asn Gly Tyr
65   70   75   80

Lys Ile Gly Leu Gly Thr Val Glu Leu Thr Thr Leu Pro Ser Leu Gly
            85   90   95

Met Val Arg Phe Lys Thr Ser Asp Phe Lys Pro Ile Ala Arg Leu Asn
            100   105   110

Ala Asp Pro Ala Ala Ile Thr Val Arg Ala Asp Ala Pro Trp Asn Ser
        115   120   125

Tyr Glu Glu Phe Met Ala Tyr Ser Lys Ala Asn Pro Gly Lys Val Arg
        130   135   140

Ile Gly Asn Ser Gly Thr Gly Ala Ile Trp His Leu Ala Ala Ala Ala
145   150   155   160

Leu Glu Asp Lys Thr Gly Thr Lys Phe Ser His Val Pro Tyr Asp Gly
                165   170   175

Ala Ala Pro Ala Ile Thr Gly Leu Leu Gly Gly His Ile Glu Ala Val
                180   185   190

Ser Val Ser Pro Gly Glu Val Ile Asn His Val Asn Gly Gly Lys Leu
        195   200   205

Lys Thr Leu Val Val Met Ala Asp Glu Arg Met Lys Thr Met Pro Asp
        210   215   220

Val Pro Thr Leu Lys Glu Lys Gly Val Asp Leu Ser Ile Gly Thr Trp
225   230   235   240

Arg Gly Leu Ile Val Ser Gln Lys Thr Pro Gln Asp Val Val Asp Val
                245   250   255

Leu Ala Lys Ala Ala Lys Glu Thr Ala Glu Glu Pro Ala Phe Gln Asp
                260   265   270

Ala Leu Gln Lys Leu Asn Leu Asn Tyr Ala Trp Leu Asp Ala Ala Ser
        275   280   285

Phe Gln Thr Gln Ile Ser Glu Gln Glu Lys Tyr Phe Asp Glu Leu Leu
        290   295   300

Thr Arg Leu Gly Leu Lys Lys
305   310

<210>   31
<211>   722
<212>   PRT

```
<213>   Escherichia coli
<400>   31

Met Leu Arg Trp Lys Arg Cys Ile Ile Leu Thr Phe Ile Ser Gly Ala
1               5                   10                  15


Ala Phe Ala Ala Pro Glu Ile Asn Val Lys Gln Asn Glu Ser Leu Pro
            20                  25                  30


Asp Leu Gly Ser Gln Ala Ala Gln Gln Asp Glu Gln Thr Asn Lys Gly
        35                  40                  45


Lys Ser Leu Lys Glu Arg Gly Ala Asp Tyr Val Ile Asn Ser Ala Thr
    50                  55                  60


Gln Gly Phe Glu Asn Leu Thr Pro Glu Ala Leu Glu Ser Gln Ala Arg
65                  70                  75                  80


Ser Tyr Leu Gln Ser Gln Ile Thr Ser Thr Ala Gln Ser Tyr Ile Glu
                85                  90                  95


Asp Thr Leu Ser Pro Tyr Gly Lys Val Arg Leu Asn Leu Ser Ile Gly
            100                 105                 110


Gln Gly Gly Asp Leu Asp Gly Ser Ser Ile Asp Tyr Phe Val Pro Trp
        115                 120                 125


Tyr Asp Asn Gln Thr Thr Val Tyr Phe Ser Gln Phe Ser Ala Gln Arg
    130                 135                 140


Lys Glu Asp Arg Thr Ile Gly Asn Ile Gly Leu Gly Val Arg Tyr Asn
145                 150                 155                 160


Phe Asp Lys Tyr Leu Leu Gly Gly Asn Ile Phe Tyr Asp Tyr Asp Phe
                165                 170                 175


Thr Arg Gly His Arg Arg Leu Gly Leu Gly Ala Glu Ala Trp Thr Asp
            180                 185                 190


Tyr Leu Lys Phe Ser Gly Asn Tyr Tyr His Pro Leu Ser Asp Trp Lys
    195                 200                 205


Asp Ser Glu Asp Phe Asp Phe Tyr Glu Glu Arg Pro Ala Arg Gly Trp
    210                 215                 220
```

```
Asp Ile Arg Ala Glu Val Trp Leu Pro Ser Tyr Pro Gln Leu Gly Gly
225                 230                 235                 240

Lys Ile Val Phe Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Gly
                245                 250                 255

Thr Asp Asn Leu Glu Lys Asp Pro Tyr Ala Val Thr Leu Gly Leu Asn
            260                 265                 270

Tyr Gln Pro Val Pro Leu Leu Thr Val Gly Thr Asp Tyr Lys Ala Gly
        275                 280                 285

Thr Gly Asp Asn Ser Asp Val Ser Ile Asn Ala Thr Leu Asn Tyr Gln
    290                 295                 300

Phe Gly Val Pro Leu Lys Asp Gln Leu Asp Ser Asp Lys Val Lys Ala
305                 310                 315                 320

Ala His Ser Leu Met Gly Ser Arg Leu Asp Phe Val Glu Arg Asn Asn
                325                 330                 335

Phe Ile Val Leu Glu Tyr Lys Glu Lys Asp Pro Leu Asp Val Thr Leu
            340                 345                 350

Trp Leu Lys Ala Asp Ala Thr Asn Glu His Pro Glu Cys Val Ile Lys
        355                 360                 365

Asp Thr Pro Glu Ala Ala Val Gly Leu Glu Lys Cys Lys Trp Thr Ile
    370                 375                 380

Asn Ala Leu Ile Asn His His Tyr Lys Ile Val Ala Ala Ser Trp Gln
385                 390             ;       395                 400

Ala Lys Asn Asn Ala Ala Arg Thr Leu Val Met Pro Val Ile Lys Glu
            405                 410                 415

Asn Thr Leu Thr Glu Gly Asn Asn Asn His Trp Asn Leu Val Leu Pro
        420                 425                 430

Ala Trp Gln Tyr Ser Ser Asp Gln Ala Glu Gln Glu Lys Leu Asn Thr
    435                 440                 445
```

```
Trp Arg Val Arg Leu Ala Leu Glu Asp Glu Lys Gly Asn Arg Gln Asn
    450                 455                 460

Ser Gly Val Val Glu Ile Thr Val Gln Gln Asp Arg Lys Ile Glu Leu
465                 470                 475                 480

Ile Val Asn Asn Ile Ala Asn Pro Glu Glu Asn Asn His Ser His Glu
                485                 490                 495

Ala Ser Ala Gln Ala Asp Gly Val Asp Gly Val Val Met Asp Leu Asp
                500                 505                 510

Val Thr Asp Ser Phe Gly Asp Asn Thr Asp Arg Asn Gly Asp Ala Leu
        515                 520                 525

Pro Glu Asp Asn Leu Thr Pro Gln Leu Tyr Asp Ala Gln Asp Lys Arg
    530                 535                 540

Val Thr Leu Thr Asn Lys Pro Cys Ser Thr Asp Asn Pro Cys Val Phe
545                 550                 555                 560

Ile Ala Lys Gln Asp Lys Glu Lys Gly Thr Val Thr Leu Ser Ser Thr
                565                 570                 575

Leu Pro Gly Thr Tyr Arg Trp Lys Ala Lys Ala Ala Pro Tyr Asp Asp
            580                 585                 590

Ser Asn Tyr Val Asp Val Thr Phe Leu Gly Ala Glu Ile Gly Gly Leu
        595                 600                 605

Asn Ala Phe Ile Tyr Arg Val Gly Ala Ala Lys Pro Ser Asn Leu Ile
    610                 615                 620

Gly Lys Asp Lys Glu Pro Leu Pro Ser Thr Thr Phe Ile Asp Leu Phe
625                 630                 635                 640

Tyr Gly Ala Thr Thr Ile Lys Thr Val Ser Ser Ser Arg Ser Lys Asn
            645                 650                 655

Leu Thr Lys Arg Trp Cys Ser Thr Thr Ser Gly Asn Leu Pro Ala
            660                 665                 670
```

Arg Ala Ser Met Val Ser Gly Cys Thr Gly Glu His Ser Asn Glu Asp
        675   680   685

Ile Val Ile Pro Ala Thr Asn Arg Glu Ala Ala Gln Thr Tyr Gly Ala
    690   695   700

Gln Ala Gly Asp Gly Leu Gln Gly Tyr Gly Leu Arg Val Leu Tyr Thr
705   710   715   720

Lys Lys

<210> 32
<211> 319
<212> PRT
<213> Escherichia coli
<400> 32

Met Lys Gln Asp Lys Arg Arg Gly Leu Thr Arg Ile Ala Leu Ala Leu
1   5   10   15

Ala Leu Ala Gly Tyr Cys Val Ala Pro Val Ala Leu Ala Glu Asp Ser
                20   25   30

Ala Trp Val Asp Ser Gly Glu Thr Asn Ile Phe Gln Gly Thr Ile Pro
            35   40   45

Trp Leu Tyr Ser Glu Gly Gly Ser Ala Thr Thr Asp Ala Asp Arg Val
    50   55   60

Thr Leu Thr Ser Asp Leu Lys Gly Ala Arg Pro Gln Gly Met Lys Arg
65   70   75   80

Thr Ser Val Phe Thr Arg Val Ile Asn Ile Gly Asp Thr Glu Gly Asp
                85   90   95

Val Asp Leu Gly Gly Leu Gly Asp Asn Ala Lys Thr Ile Asp Thr Ile
            100   105   110

Arg Trp Met Ser Tyr Lys Asp Ala Gln Gly Gly Asp Pro Lys Glu Leu
        115   120   125

Ala Thr Lys Val Thr Ser Tyr Thr Leu Thr Asp Ala Asp Arg Gly Arg
    130   135   140

Tyr Ile Gly Ile Glu Ile Thr Pro Thr Thr Gln Thr Gly Thr Pro Asn
145   150   155   160

Val Gly Thr Ala Leu His Leu Tyr Asp Val Ser Thr Ala Ser Gly Gly
                165   170   175

Gly Ser Asp Ser Asp Asn Val Ala Pro Gly Pro Val Val Asn Gln Asn
            180   185   190

Leu Lys Val Ala Ile Phe Val Asp Gly Thr Ser Ile Asn Leu Ile Asn
        195   200   205

Gly Ser Thr Pro Ile Glu Leu Gly Lys Thr Tyr Val Ala Lys Leu Tyr
    210   215   220

Ser Asp Glu Asn Lys Asn Gly Lys Phe Asp Ala Gly Thr Asp Ala Asp
225   230   235   240

Val Thr Ala Asn Tyr Asp Phe Arg Trp Val Leu Ser Gly Ser Ser Gln
            245   250   255

Gln Leu Gly Thr Ser Gly Gly Ile Val Asn Ser Ser Phe Asp Asn Asn
        260   265   270

Asn Leu Val Ile Pro Ala Thr Asn Asp Glu Ala Arg Thr Asn Leu Asn
        275   280   285

Gly Pro Ala Arg Asp Gly Lys Glu Ala Leu Ser Ile Pro Thr Asn Gly
    290   295   300

Asp Gly Val Gln Gly Tyr Lys Leu His Ile Ile Tyr Lys His Lys
305   310   315

<210>   33
<211>   629
<212>   PRT
<213>   Escherichia coli
<400>   33

Met Lys Lys Val Leu Thr Leu Ser Leu Leu Ala Leu Cys Val Ser His
1   5   10   15

Ser Ala Val Ala Ala Asn Tyr Thr Phe Asn Asn Asp Asn Ile Ala Leu
        20   25   30

Ser Phe Asp Asp Thr Asn Ser Thr Ile Val Leu Lys Asp Arg Arg Thr
        35   40   45

Asn His Pro Ile Thr Pro Gln Glu Leu Phe Phe Leu Thr Leu Pro Asp
        50   55   60

Glu Thr Lys Ile His Thr Ala Asp Phe Lys Ile Lys His Ile Lys Lys
65   70   75   80

Gln Asp Asn Ala Ile Val Ile Asp Phe Thr Arg Pro Asp Phe Asn Val
                85   90   95

Thr Val Gln Leu Asn Leu Val Lys Gly Lys Tyr Ala Ser Ile Asp Tyr
            100   105   110

Thr Ile Ala Ala Val Gly Gln Pro Arg Asp Val Ala Lys Ile Thr Phe
        115   120   125

Phe Pro Thr Lys Lys Gln Phe Gln Ala Pro Tyr Val Asp Gly Ala Ile
    130   135   140

Thr Ser Ser Pro Ile Ile Ala Asp Ser Phe Phe Ile Leu Pro Asn Lys
145   150   155   160

Pro Ile Val Asn Thr Tyr Ala Tyr Glu Ala Thr Thr Asn Leu Asn Val
                165   170   175

Glu Leu Lys Thr Pro Ile Gln Pro Glu Thr Pro Val Ser Phe Thr Thr
            180   185   190

Trp Phe Gly Thr Phe Pro Glu Thr Ser Gln Leu Arg Arg Ser Val Asn
        195   200   205

Gln Phe Ile Asn Ala Val Arg Pro Arg Pro Tyr Lys Pro Tyr Leu His
    210   215   220

Tyr Asn Ser Trp Met Asp Ile Gly Phe Phe Thr Pro Tyr Thr Glu Gln
225   230   235   240

Asp Val Leu Gly Arg Met Asp Glu Trp Asn Lys Glu Phe Ile Ser Gly
            245   250   255

```
Arg Gly Val Ala Leu Asp Ala Phe Leu Leu Asp Asp Gly Trp Asp Asp
            260             265             270

Leu Thr Gly Arg Trp Leu Phe Gly Pro Ala Phe Ser Asn Gly Phe Ser
            275             280             285

Lys Val Arg Glu Lys Ala Asp Ser Leu His Ser Ser Val Gly Leu Trp
            290             295             300

Leu Ser Pro Trp Gly Gly Tyr Asn Lys Pro Gln Arg Arg Ser Arg Phe
305             310             315             320

Ala Cys Lys Arg Val Trp Val Arg Asn Arg Gly Arg Gln Ala Gly Ala
            325             330             335

Phe Gly Ser Glu Leu Leu Lys Asn Phe Asn Glu Gln Ile Ile Asn Leu
            340             345             350

Ile Lys Asn Glu His Ile Thr Ser Phe Lys Leu Asp Gly Met Gly Asn
            355             360             365

Ala Ser Ser His Ile Lys Gly Ser Pro Phe Ala Ser Asp Phe Asp Ala
            370             375             380

Ser Ile Ala Leu Leu His Asn Met Arg Arg Ala Asn Pro Asn Leu Phe
385             390             395             400

Ile Asn Leu Thr Thr Gly Thr Asn Ala Ser Pro Ser Trp Leu Phe Tyr
            405             410             415

Ala Asp Ser Ile Trp Arg Gln Gly Asp Asp Ile Asn Leu Tyr Gly Pro
            420             425             430

Gly Thr Pro Val Gln Gln Trp Ile Thr Tyr Arg Asp Ala Glu Thr Tyr
            435             440             445

Arg Ser Ile Val Arg Lys Gly Pro Leu Phe Pro Leu Asn Ser Leu Met
            450             455             460

Tyr His Gly Ile Val Ser Ala Glu Asn Ala Tyr Tyr Gly Leu Glu Lys
465             470             475             480
```

Val Gln Thr Asp Ser Asp Phe Ala Asp Gln Val Trp Ser Tyr Phe Ala
            485   490   495

Thr Gly Thr Gln Leu Gln Glu Leu Tyr Ile Thr Pro Ser Met Leu Asn
            500   505   510

Lys Val Lys Trp Asp Thr Leu Ala Lys Ala Ala Lys Trp Ser Lys Glu
            515   520   525

Asn Ala Ser Val Leu Val Asp Thr His Trp Ile Gly Gly Asp Pro Thr
    530   535   540

Ala Leu Ala Val Tyr Gly Trp Ala Ser Trp Ser Lys Asp Lys Ala Ile
545   550   555   560

Leu Gly Leu Arg Asn Pro Ser Asp Lys Pro Gln Thr Tyr Tyr Leu Asp
            565   570   575

Leu Ala Lys Asp Phe Glu Ile Pro Ala Gly Asn Ala Ala Gln Phe Ser
            580   585   590

Leu Lys Ala Val Tyr Gly Ser Asn Lys Thr Val Pro Val Glu Tyr Lys
            595   600   605

Asn Ala Thr Val Ile Thr Leu Gln Pro Leu Glu Thr Leu Val Phe Glu
    610   615   620

Ala Val Thr Ile Asn
625

<210>   34
<211>   1778
<212>   PRT
<213>   Escherichia coli
<400>   34

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr
1   5   10   15

Thr Val Ala Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
            20   25   30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Leu Leu Ser Ser
            35   40   45

```
Phe Gly Ala Ser Ala Asp Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly
    50              55              60

Asp Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly Ala Lys
65              70              75              80

Ala Asn Thr Phe Met Asn Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr
            85              90              95

Asp Ala Ile Ala Glu Gly Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr
            100             105             110

Leu Ala Thr Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala Lys Ala
        115             120             125

Met Gly Asp Arg Ser Val Ala Leu Gly Ala Ser Ser Val Ala Asn Gly
    130             135             140

Asp Arg Ser Met Ala Phe Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr
145             150             155             160

Ser Leu Ala Ile Gly Asp Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile
            165             170             175

Ala Leu Gly Asn Thr Ala Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu
            180             185             190

Gly Asp Asn Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala
        195             200             205

Ser Ser Lys Ala Gly Gly Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser
    210             215             220

Thr Ala Asn Ser Thr Gly Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser
225             230             235             240

Ser Asn Asp Asn Ala Ile Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly
            245             250             255

Val Asn Ser Met Ala Leu Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser
            260             265             270
```

```
Ser Ile Ala Leu Gly Asn Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile
    275                 280                 285

Ala Leu Gly Gln Gly Ser Ile Ala Ser Lys Val Asn Ser Ile Ala Leu
    290                 295                 300

Gly Ser Asn Ser Leu Ser Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu
305                 310                 315                 320

Gly Ser Ala Ala Gly Gly Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser
                325                 330                 335

Arg Ala Asn Gly Asn Asp Ser Val Ala Ile Gly Val Gly Ala Ala Ala
                340                 345                 350

Ala Thr Asp Asn Ser Val Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala
    355                 360                 365

Ser Asn Thr Val Ser Val Gly Asn Ser Ala Thr Lys Arg Lys Ile Val
    370                 375                 380

Asn Met Ala Ala Gly Ala Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn
385                 390                 395                 400

Gly Ser Gln Leu Tyr Thr Ile Ser Asp Ser Val Ala Lys Arg Leu Gly
                405                 410                 415

Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala Val Ser Tyr
            420                 425                 430

Ala Leu Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly
    435                 440                 445

Ile Asp Asn Asn Thr Leu Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser
    450                 455                 460

Ala Asn His Gly Ala Asn Ala Thr Asn Lys Ile Thr Asn Val Ala Lys
465                 470                 475                 480

Gly Thr Val Ser Ala Thr Ser Thr Asp Val Val Asn Gly Ser Gln Leu
                485                 490                 495

Tyr Asp Leu Gln Gln Asp Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser
```

```
                500                   505                   510


Ala Ala His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala
        515              520              525


Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu
        530              535              540


Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Asn Ile Ala Thr
545              550              555              560


Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly
            565              570              575


Asp Asp Ser Leu Leu Trp Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala
            580              585              590


His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn
        595              600              605


Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr
    610              615              620


Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr
625              630              635              640


Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp
            645              650              655


Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly
            660              665              670


Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr
        675              680              685


Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn
    690              695              700


Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn
705              710              715              720


Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu
            725              730              735
```

```
Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp
            740             745             750

Ala Thr Ser Lys Ile Thr Asn Val Lys Ala Gly Asp Leu Thr Ala Gly
            755             760             765

Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn
            770             775             780

Val Ser Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn
785             790             795             800

Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe
            805             810             815

Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys
            820             825             830

Ala Gly Asp Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln
            835             840             845

Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Ile Thr
850             855             860

Asn Leu Thr Asp Ser Val Gly Asp Leu Lys Asp Asp Ser Leu Leu Trp
865             870             875             880

Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr
            885             890             895

Ser Lys Ile Thr Asn Leu Leu Ala Gly Lys Ile Ser Ser Asn Ser Thr
            900             905             910

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val Ala Asp Ser Phe Thr
            915             920             925

Ser Tyr Leu Gly Gly Gly Ala Asp Ile Ser Asp Thr Gly Val Leu Ser
            930             935             940

Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp
945             950             955             960
```

Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr Ser Leu Gly Asp Ala
            965   970   975

Leu Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Ile
            980   985   990

Asn Asn Ala Pro Ser Val Ile Thr Asp Val Ala Asn Gly Ala Val Ser
            995   1000   1005

Ser Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val
    1010   1015   1020

Ser Asp Tyr Ile Ala Asp Ala Leu Gly Gly Asn Ala Val Val Asn
    1025   1030   1035

Thr Asp Gly Ser Ile Thr Thr Pro Thr Tyr Ala Ile Ala Gly Gly
    1040   1045   1050

Ser Tyr Asn Asn Val Gly Asp Ala Leu Glu Ala Ile Asp Thr Thr
    1055   1060   1065

Leu Asp Asp Ala Leu Leu Trp Asp Thr Thr Ala Asn Gly Gly Asn
    1070   1075   1080

Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val
    1085   1090   1095

Ile Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp
    1100   1105   1110

Ala Ile Asn Gly Ser Gln Leu Tyr Ser Thr Asn Lys Tyr Ile Ala
    1115   1120   1125

Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile
    1130   1135   1140

Thr Ala Pro Thr Tyr Thr Ile Ala Asn Thr Asp Tyr Asn Asn Val
    1145   1150   1155

Gly Glu Ala Leu Asp Ala Leu Asp Asn Asn Ala Leu Leu Trp Asp
    1160   1165   1170

Glu	Asp	Ala	Gly	Ala	Tyr	Asn	Ala	Ser	His	Asp	Gly	Asn	Ala	Ser
1175					1180					1185				

Lys	Ile	Thr	Asn	Val	Ala	Ala	Gly	Asp	Leu	Ser	Thr	Thr	Ser	Thr
1190					1195					1200				

Asp	Ala	Val	Asn	Gly	Ser	Gln	Leu	Asn	Ala	Thr	Asn	Ile	Leu	Val
1205					1210					1215				

Thr	Gln	Asn	Ser	Gln	Met	Ile	Asn	Gln	Leu	Ala	Gly	Asn	Thr	Ser
1220					1225					1230				

Glu	Thr	Tyr	Ile	Glu	Glu	Asn	Gly	Ala	Gly	Ile	Asn	Tyr	Val	Arg
1235					1240					1245				

Thr	Asn	Asp	Ser	Gly	Leu	Ala	Phe	Asn	Asp	Ala	Ser	Ala	Ser	Gly
1250					1255					1260				

Ile	Gly	Ala	Thr	Ala	Val	Gly	Tyr	Asn	Ala	Val	Ala	Ser	His	Ala
1265					1270					1275				

Ser	Ser	Val	Ala	Ile	Gly	Gln	Asp	Ser	Ile	Ser	Glu	Val	Asp	Thr
1280					1285					1290				

Gly	Ile	Ala	Leu	Gly	Ser	Ser	Ser	Val	Ser	Ser	Arg	Val	Ile	Val
1295					1300					1305				

Lys	Gly	Thr	Arg	Asn	Thr	Ser	Val	Ser	Glu	Glu	Gly	Val	Val	Ile
1310					1315					1320				

Gly	Tyr	Asp	Thr	Thr	Asp	Gly	Glu	Leu	Leu	Gly	Ala	Leu	Ser	Ile
1325					1330					1335				

Gly	Asp	Asp	Gly	Lys	Tyr	Arg	Gln	Ile	Ile	Asn	Val	Ala	Asp	Gly
1340					1345					1350				

Ser	Glu	Ala	His	Asp	Ala	Val	Thr	Val	Arg	Gln	Leu	Gln	Asn	Ala
1355					1360					1365				

Ile	Gly	Ala	Val	Ala	Thr	Thr	Pro	Thr	Lys	Tyr	Tyr	His	Ala	Asn
1370					1375					1380				

Ser	Thr	Ala	Glu	Asp	Ser	Leu	Ala	Val	Gly	Glu	Asp	Ser	Leu	Ala

81

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        1385                1390                1395


Met Gly Ala Lys Thr Ile Val  Asn Gly Asn Ala Gly  Ile Gly Ile
    1400                1405                1410


Gly Leu Asn Thr Leu Val Leu  Ala Asp Ala Ile Asn  Gly Ile Ala
    1415                1420                1425


Ile Gly Ser Asn Ala Arg Ala  Asn His Ala Asp Ser  Ile Ala Met
    1430                1435                1440


Gly Asn Gly Ser Gln Thr Thr  Arg Gly Ala Gln Thr  Asn Tyr Thr
    1445                1450                1455


Ala Tyr Asn Met Asp Ala Pro  Gln Asn Ser Val Gly  Glu Phe Ser
    1460.               1465                1470


Val Gly Ser Glu Asp Gly Gln  Arg Gln Ile Thr Asn  Val Ala Ala
    1475                1480                1485


Gly Ser Ala Asp Thr Asp Ala  Val Asn Val Gly Gln  Leu Lys Val
    1490                1495                1500


Thr Asp Ala Gln Val Ser Gln  Asn Thr Gln Ser Ile  Thr Asn Leu
    1505                1510                1515


Asn Thr Gln Val Thr Asn Leu  Asp Thr Arg Val Thr  Asn Ile Glu
    1520                1525                1530


Asn Gly Ile Gly Asp Ile Val  Thr Thr Gly Ser Thr  Lys Tyr Phe
    1535                1540                1545


Lys Thr Asn Thr Asp Gly Ala  Asp Ala Asn Ala Gln  Gly Lys Asp
    1550                1555                1560


Ser Val Ala Ile Gly Ser Gly  Ser Ile Ala Ala Ala  Asp Asn Ser
    1565                1570                1575


Val Ala Leu Gly Thr Gly Ser  Val Ala Asp Glu Glu  Asn Thr Ile
    1580                1585                1590


Ser Val Gly Ser Ser Thr Asn  Gln Arg Arg Ile Thr  Asn Val Ala
    1595                1600                1605
```

```
Ala Gly  Val Asn Ala Thr Asp  Ala Val Asn Val Ser  Gln Leu Lys
    1610             1615             1620


Ser Ser  Glu Ala Gly Gly Val  Arg Tyr Asp Thr Lys  Ala Asp Gly
    1625             1630             1635


Ser Ile  Asp Tyr Ser Asn Ile  Thr Leu Gly Gly Gly  Asn Ser Gly
    1640             1645             1650


Thr Thr  Arg Ile Ser Asn Val  Ser Ala Gly Val Asn  Asn Asn Asp
    1655             1660             1665


Ala Val  Asn Tyr Ala Gln Leu  Lys Gln Ser Val Gln  Glu Thr Lys
    1670             1675             1680


Gln Tyr  Thr Asp Gln Arg Met  Val Glu Met Asp Asn  Lys Leu Ser
    1685             1690             1695


Lys Thr  Glu Ser Lys Leu Ser  Gly Gly Ile Ala Ser  Ala Met Ala
    1700             1705             1710


Met Thr  Gly Leu Pro Gln Ala  Tyr Thr Pro Gly Ala  Ser Met Ala
    1715             1720             1725


Ser Ile  Gly Gly Gly Thr Tyr  Asn Gly Glu Ser Ala  Val Ala Leu
    1730             1735             1740


Gly Val  Ser Met Val Ser Ala  Asn Gly Arg Trp Val  Tyr Lys Leu
    1745             1750             1755


Gln Gly  Ser Thr Asn Ser Gln  Gly Glu Tyr Ser Ala  Ala Leu Gly
    1760             1765             1770


Ala Gly  Ile Gln Trp
    1775


<210>  35
<211>  227
<212>  PRT
<213>  Escherichia coli
<400>  35

Met Asn Leu Lys Lys Thr Leu Leu Ser Val Leu Met Ile Leu Gln Leu
```

				5					10					15	

Cys Leu Leu Val Gly Cys Asp Tyr Ile Glu Lys Ala Ser Lys Val Asp
               20   25   30

Asp Leu Val Thr Gln Gln Glu Leu Gln Lys Ser Lys Ile Glu Ala Leu
           35   40   45

Glu Lys Gln Gln Glu Leu Asp Lys Arg Lys Ile Glu His Phe Glu Lys
      50   55   60

Gln Gln Thr Thr Ile Ile Asn Ser Thr Lys Thr Leu Ala Gly Val Val
65   70   75   80

Lys Ala Val Lys Asn Lys Gln Asp Glu Phe Val Phe Thr Glu Phe Asn
             85   90   95

Pro Ala Gln Thr Gln Tyr Phe Ile Leu Asn Asn Gly Ser Val Gly Leu
            100   105   110

Ala Gly Lys Ile Leu Ser Ile Asp Ala Val Glu Asn Gly Ser Val Ile
          115   120   125

Arg Ile Ser Leu Val Asn Leu Leu Ser Val Pro Val Ser Asn Met Gly
      130   135   140

Phe Tyr Ala Thr Trp Gly Gly Glu Lys Pro Thr Asp Ile Asn Ala Leu
145   150   155   160

Ala Lys Trp Gln Gln Leu Leu Phe Ser Thr Ala Met Asn Ser Ser Leu
            165   170   175

Lys Leu Leu Pro Gly Gln Trp Gln Asp Ile Asn Leu Thr Leu Lys Gly
          180   185   190

Val Ser Pro Asn Asn Leu Lys Tyr Leu Lys Leu Ala Ile Asn Met Ala
           195   200   205

Asn Ile Gln Phe Asp Arg Leu Gln Pro Ala Glu Ser Pro Gln Arg Lys
      210   215   220

Asn Lys Lys
225

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<210>   36
<211>   1109
<212>   PRT
<213>   Escherichia coli
<400>   36
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Met Lys Arg Val Val Arg Leu Leu Gly Val Gly Leu Leu Leu Val
1   5   10   15

Val Leu Leu Leu Ile Leu Phe Val Leu Ala Gln Thr Thr Pro Leu Ile
            20   25   30

Ser Ala Gln Asp Glu His Ala Val Trp Leu Arg Leu Leu Ile Thr Ala
            35   40   45

Ile Val Ile Cys Leu Leu Ser Met Cys Ile Phe Phe Leu Phe Ser Phe
    50   55   60

Arg Gln Asn Glu Ala Ser Thr Ile Ser Leu Tyr Ala Gln Pro Thr Asp
65   70   75   80

Ile Lys Glu Ile Asn Thr Glu Gln Pro Asn Tyr Ala Ser Leu Leu Thr
                85   90   95

Ile Tyr Leu Arg Asp Arg Tyr Gly Pro Phe Trp Arg Arg Lys Val Arg
            100   105   110

Leu Leu Leu Val Thr Gly Glu Pro Glu Gln Ala Glu Ala Ile Ala Pro
        115   120   125

Gly Leu Thr Gly Gln His Trp Leu Glu Gly Asp His Thr Val Leu Ile
    130   135   140

Tyr Gly Gly Arg Pro Thr Ala Glu Pro Asp Val Thr Leu Leu Thr Ala
145   150   155   160

Leu Lys Lys Leu Arg Arg Ser Arg Pro Leu Asp Gly Ile Ile Trp Ala
                165   170   175

Leu Thr Glu Glu Gln Ser Arg Gln Thr Ala Gln Leu Asp Lys Gly Trp
                180   185   190

Arg Gly Leu Ile Asn Gly Gly Lys Arg Leu Gly Phe Gln Ala Pro Leu
```

```
            195                    200                    205

Tyr Leu Trp Gln Val Cys Asp Asp Gly Asp Tyr Gln Thr Gly Arg Pro
    210             215             220

Leu Gln Ser Val Gly Cys Leu Leu Pro Glu Arg Cys Thr Pro Glu Gln
225             230             235             240

Leu Ala Val Met Leu Glu Ala Ala Ala Asp Gly Thr Gly His Val Ala
            245             250             255

Ala Thr Asp Arg Tyr Arg Met Phe Ser Ala Ala Ser Gly Ser Tyr Pro
            260             265             270

Cys Arg Ala Gly Tyr Cys Ser Leu Ala Asp Arg Pro Glu Thr Ala Ala
        275             280             285

Gly Arg Arg Arg Ile Phe Phe Pro Ala Pro Ala Arg Pro Asp Val Gln
    290             295             300

Pro Ala Ala Cys Arg Arg Ala Gly Gly Gln His Leu Met Gln Trp Leu
305             310             315             320

Pro Ser Pro Val Trp Ala Gly Val Thr Val Ile Thr Arg Ala Gly Ala
            325             330             335

Arg Trp Val Phe Leu Trp Leu Arg Thr Ala Leu Met Ser Ala Val Cys
            340             345             350

Val Leu Val Ile Trp Gly Ala Gly Met Thr Thr Ser Phe Phe Ala Asn
        355             360             365

Arg Ala Leu Val Gln Glu Thr Gly Ile Gln Thr Ala Arg Ala Leu Asp
    370             375             380

Thr Arg Leu Pro Leu Ala Glu Gln Leu Val Ala Leu His Thr Leu Gln
385             390             395             400

Gly Glu Leu Glu Arg Leu Gln Tyr Arg Ile Arg Glu Gly Ala Pro Trp
                405             410             415

Tyr Gln Arg Phe Gly Leu Glu Arg Asn Gln Gln Leu Leu Ala Ala Ala
            420             425             430
```

```
Phe Pro Gly Tyr Ala Gln Ala Ala Asn Arg Leu Val Arg Asp Val Ala
    435             440             445

Val Asp His Leu Gln Gln Gln Leu Asn Ala Phe Val Ala Leu Pro Pro
    450             455             460

Asn Ser Pro Gln Arg Thr Ala Thr Gly Glu Gln Arg Tyr Lys Gln Leu
465             470             475             480

Lys Ala Leu Leu Met Thr Ser Arg Pro Glu Lys Ala Asp Ala Ala Phe
            485             490             495

Phe Ser Thr Thr Leu Met Ala Asp Gly Leu Arg Tyr Glu Asn Ile Pro
        500             505             510

Glu Gly Val Arg Gln Ser Val Leu Pro Ser Leu Leu Thr Phe Trp Thr
        515             520             525

Ala Asn Leu Pro Glu His Pro Gln Trp Lys Thr Ser Pro Pro Pro Glu
    530             535             540

Leu Thr Gly Ala Val Arg Lys Ile Leu Leu Arg Gln Ile Gly Val Arg
545             550             555             560

Asn Ala Glu Asn Thr Leu Tyr Gln Asn Val Leu Gln Gln Val Ser Arg
            565             570             575

Asn Tyr Ala Asp Met Thr Leu Ala Asp Met Thr Gly Asp Thr Leu Thr
            580             585             590

Glu Ser Leu Phe Ser Thr Glu Gln Thr Val Pro Gly Met Phe Thr Arg
        595             600             605

Gln Ala Trp Glu Gly Gln Val Arg Glu Ala Ile Glu Gln Val Val Thr
    610             615             620

Ala Arg Arg Glu Glu Ile Asp Trp Val Leu Ser Asp Arg Gln Gln Asp
625             630             635             640

Thr Ser Ala Asp Ile Ser Pro Asp Thr Leu Arg Asn Arg Leu Thr Ser
            645             650             655
```

Arg Tyr Phe Thr Asp Phe Ala Gly Ser Trp Leu Ala Phe Leu Asn Ser
              660   665   670

Ile His Trp Lys Lys Glu Asp Ser Leu Ser Gly Ile Leu Asp Gln Leu
          675   680   685

Thr Leu Met Ala Asp Ala Arg Gln Ser Pro Leu Ile Ala Leu Thr Asp
          690   695   700

Thr Leu Ala Trp Gln Ala Ala Thr Gly Arg Glu Asn Arg Gly Leu Ser
705   710   715   720

Asp Ser Leu Ala Lys Ser Ala Gln Glu Leu Phe Asn Gly Lys Glu Lys
              725   730   735

Thr Pro Gln Gln Ser Arg Glu Gly Asp Asp Val Pro Val Gly Pro Leu
              740   745   750

Asp Lys Thr Phe Thr Pro Leu Leu Arg Leu Leu Gly Asp Lys Ala Gly
          755   760   765

Gly Gly Asp Ser Gln Leu Ser Leu Gln Thr Tyr Leu Thr Arg Val Thr
    770   775   780

Arg Val Arg Leu Lys Leu Gln Gln Val Thr Asn Ala Pro Asp Pro Gln
785   790   795   800

Glu Met Thr Gln Gln Leu Ala Gln Thr Val Leu Gln Gly Lys Thr Val
              805   810   815

Asp Leu Thr Asp Thr Arg Asp Tyr Gly Arg Leu Ile Ala Ala Ser Leu
              820   825   830

Gly Glu Glu Trp Ser Gly Phe Gly Gln Ala Leu Phe Val Arg Pro Val
    835   840   845

Glu Gln Ser Trp Arg Gln Val Leu Thr Pro Ala Ala Asp Ser Leu Asn
    850   855   860

Arg Gln Trp Gln Arg Ala Ile Val Ser His Trp Asn Gln Asp Phe Ala
865   870   875   880

```
Gly Arg Tyr Pro Phe Lys Ala Ser Gln Asn Asp Ala Ser Leu Pro Leu
            885                 890                 895

Leu Ala Gln Tyr Leu Arg Asp Asp Gly Arg Ile Asn Leu Phe Ile Ala
            900                 905                 910

Ala Asn Leu Ser Gly Val Leu Lys Arg Glu Gly Arg Tyr Trp Val Ala
            915                 920                 925

Asp Ala Met Asn Thr Gln Gly Leu Thr Val Asn Pro Asp Phe Ile Arg
    930                 935                 940

Ala Leu Asn Arg Leu Arg Asp Val Ala Asp Thr Ala Phe Ala Ser Gly
945                 950                 955                 960

Asp Ala Gly Ile His Phe Glu Leu Arg Ala Lys Pro Ala Arg Asp Val
            965                 970                 975

Met Lys Thr His Leu Val Ile Asp Gly Gln Glu Leu Glu Tyr Phe Asn
            980                 985                 990

Gln Lys Glu Arg Trp Gln Arg Phe  Asn Trp Pro Asp Glu  Gln Trp Gln
            995                 1000                1005

Pro Gly  Ala Ser Leu Ser Trp  Thr Ser Thr Gln Ala  Met Glu Arg
    1010                1015                1020

Ile Leu  Ala Asp Tyr Arg Gly  Ser Trp Ser Leu Ile  Arg Leu Leu
    1025                1030                1035

Glu Gln  Ala Gln Val Thr Pro  Val Asp Ser Ser Thr  Phe Lys Val
    1040                1045                1050

Val Trp  Lys Ala Gln Asp Gly  Leu Pro Leu Asn Tyr  Leu Leu Arg
    1055                1060                1065

Val Glu  Gln Gly Lys Gly Pro  Leu Ala Leu Leu Glu  Leu Lys Asn
    1070                1075                1080

Phe Arg  Leu Pro Gly Gln Val  Phe Leu Thr Gly Lys  Ser Met Lys
    1085                1090                1095

Asp Val  Glu Glu Tyr Gly Glu  Asp Ala Asp Glu
```

<210> 37
<211> 178
<212> PRT
<213> Escherichia coli
<400> 37

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
1   5   10   15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
                20   25   30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
        35   40   45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
    50   55   60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
65   70   75   80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
                85   90   95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
            100   105   110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
            115   120   125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
        130   135   140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
145   150   155   160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
                165   170   175

Asp Lys

```
<210>    38
<211>    280
<212>    PRT
<213>    Escherichia coli
<400>    38
```

Met Ile Ser Gly Gly Asn Met Leu Lys Glu Trp Met Ile Phe Thr Cys
1   5   10   15

Ser Leu Leu Thr Leu Ala Gly Ala Ser Leu Pro Leu Ser Gly Cys Ile
            20   25   30

Ser Arg Gly Gln Glu Ser Ile Ser Glu Gly Ala Ala Phe Gly Ala Gly
        35   40   45

Ile Leu Arg Glu Pro Gly Ala Thr Lys Lys Ala Asp Thr Lys Asp Leu
    50   55   60

Asn Val Pro Pro Pro Val Tyr Gly Pro Pro Gln Val Ile Phe Arg Ile
65   70   75   80

Asp Asp Asn Arg Tyr Phe Thr Leu Glu Asn Tyr Thr His Cys Glu Asn
            85   90   95

Gly Gln Thr Phe Tyr Asn Asn Lys Ala Lys Asn Ile His Val Lys Ile
            100   105   110

Leu Asp Ala Ser Gly Tyr Leu Phe Lys Gly Arg Leu Phe Trp Leu Ser
            115   120   125

Thr Arg Asp Asp Phe Leu Ala Phe Pro Ala Thr Leu Asn Thr Arg His
    130   135   140

Ala Ser Cys Met Gly Ser Asn Lys Gly Cys Met Asn Ala Val Ile Val
145   150   155   160

Thr Thr Asp Gly Gly Lys Arg Arg Ser Gly Val Pro Tyr Gly Ser Tyr
            165   170   175

Thr Gln Asn Pro Thr Gly Ala Thr Arg Asp Tyr Asp Met Leu Val Met
            180   185   190

Asn Asp Gly Phe Tyr Leu Leu Arg Tyr Arg Gly Gly Gln Gly Arg Phe
            195   200   205

```
Ser Pro Val Ile Leu Arg Trp Ile Leu Ser Thr Glu Asp Ser Ser Gly
    210             215             220
```

```
Val Val Arg Ser Glu Asp Ala Tyr Glu Leu Phe Arg Pro Gly Glu Glu
225             230             235             240
```

```
Val Pro Ser Thr Gly Phe Tyr Lys Ile Asp Leu Ser Arg Phe Tyr Pro
            245             250             255
```

```
Lys Asn Asn Val Met Glu Met Gln Cys Asp Arg Thr Leu Glu Pro Val
            260             265             270
```

```
Gln Pro Ser Glu Ser Lys Ile Gln
        275             280
```

<210> 39
<211> 501
<212> PRT
<213> Escherichia coli
<400> 39

```
Met Glu His Val Ser Ile Lys Thr Leu Tyr His Leu Leu Cys Cys Met
1               5               10              15
```

```
Leu Leu Phe Ile Ser Ala Met Cys Ala Leu Ala Gln Glu His Glu Pro
            20              25              30
```

```
Ile Gly Ala Gln Asp Glu Arg Leu Ser Thr Leu Ile His Gln Arg Met
        35              40              45
```

```
Gln Glu Ala Lys Val Pro Ala Leu Ser Val Ser Val Thr Ile Lys Gly
    50              55              60
```

```
Val Arg Gln Arg Phe Val Tyr Gly Val Ala Asp Val Ala Ser Gln Lys
65              70              75              80
```

```
Ala Asn Thr Leu Asp Thr Val Tyr Glu Leu Gly Ser Met Ser Lys Ala
            85              90              95
```

```
Phe Thr Gly Leu Val Val Gln Ile Leu Ile Gln Glu Gly Arg Leu Arg
            100             105             110
```

```
Gln Gly Asp Asp Ile Ile Thr Tyr Leu Pro Glu Met Arg Leu Asn Tyr
        115             120             125
```

```
Gln Gly Lys Pro Ala Ser Leu Thr Val Ala Asp Phe Leu Tyr His Thr
    130             135             140

Ser Gly Leu Pro Phe Ser Thr Leu Ala Arg Leu Glu Asn Pro Met Pro
145             150             155             160

Gly Ser Ala Val Ala Gln Gln Leu Arg Asn Glu Asn Leu Leu Phe Ala
                165             170             175

Pro Gly Ala Lys Phe Ser Tyr Ala Ser Ala Asn Tyr Asp Val Leu Gly
            180             185             190

Ala Val Ile Glu Asn Val Thr Gly Lys Thr Phe Thr Glu Val Ile Ala
        195             200             205

Glu Arg Leu Thr Gln Pro Leu Gly Met Ser Ala Thr Val Ala Val Lys
    210             215             220

Gly Asp Glu Ile Ile Val Asn Lys Ala Ser Gly Tyr Lys Leu Gly Phe
225             230             235             240

Gly Lys Pro Val Leu Phe His Ala Pro Leu Ala Arg Asn His Val Pro
            245             250             255

Ala Ala Tyr Ile His Ser Thr Leu Pro Asp Met Glu Ile Trp Ile Asp
        260             265             270

Ala Trp Leu His Arg Lys Ala Leu Pro Ala Thr Leu Arg Glu Ala Met
    275             280             285

Ser Asn Ser Trp Arg Gly Asn Ser Asp Val Pro Leu Ala Ala Asp Asn
290             295             300

Arg Ile Leu Tyr Ala Ser Gly Trp Phe Ile Asp Gln Asn Gln Gly Pro
305             310             315             320

Tyr Ile Ser His Gly Gly Gln Asn Pro Asn Phe Ser Ser Cys Ile Ala
            325             330             335

Leu Arg Pro Asp Gln Gln Ile Gly Ile Val Ala Leu Ala Asn Met Asn
            340             345             350
```

```
Ser Asn Leu Ile Leu Gln Leu Cys Ala Asp Ile Asp Asn Tyr Leu Arg
        355                 360                 365

Ile Gly Lys Tyr Ala Asp Gly Ala Gly Asp Ala Ile Thr Ala Thr Asp
        370                 375                 380

Thr Leu Phe Val Tyr Leu Thr Leu Leu Leu Cys Phe Trp Gly Ala Val
385                 390                 395                 400

Val Val Val Arg Gly Ala Phe Arg Val Tyr Arg Ala Thr Ala His Gly
                405                 410                 415

Pro Gly Lys Gln Gln Arg Leu Arg Leu Arg Val Arg Asp Tyr Ile Ile
        420                 425                 430

Ala Leu Ala Val Pro Gly Leu Val Ala Ala Met Leu Tyr Val Ala Pro
        435                 440                 445

Gly Ile Leu Ser Pro Gly Leu Asp Trp Arg Phe Ile Leu Val Trp Gly
        450                 455                 460

Pro Ser Ser Val Leu Ala Ile Pro Phe Gly Ile Ile Leu Leu Ala Phe
465                 470                 475                 480

Val Leu Thr Leu Asn His Gln Ile Lys Arg Ile Leu Leu His Asn Lys
                485                 490                 495

Glu Trp Asp Asp Glu
        500
```

```
<210>   40
<211>   682
<212>   PRT
<213>   Escherichia coli
<400>   40
```

```
Met Lys Asn Lys Tyr Ile Ile Ala Pro Gly Ile Ala Val Met Cys Ser
1               5                   10                  15

Ala Val Ile Ser Ser Gly Tyr Ala Ser Ser Asp Lys Lys Glu Asp Thr
        20                  25                  30

Leu Val Val Thr Ala Ser Gly Phe Thr Gln Gln Leu Arg Asn Ala Pro
        35                  40                  45
```

```
Ala Ser Val Ser Val Ile Thr Ser Glu Gln Leu Gln Lys Lys Pro Val
    50                  55                  60

Ser Asp Leu Val Asp Ala Val Lys Asp Val Glu Gly Ile Ser Ile Thr
65              70                  75                  80

Gly Gly Asn Glu Lys Pro Asp Ile Ser Ile Arg Gly Leu Ser Gly Asp
                85                  90                  95

Tyr Thr Leu Ile Leu Val Asp Gly Arg Arg Gln Ser Gly Arg Glu Ser
            100                 105                 110

Arg Pro Asn Gly Ser Gly Gly Phe Glu Ala Gly Phe Ile Pro Pro Val
        115                 120                 125

Glu Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met Ser Ser Leu
    130                 135                 140

Tyr Gly Ser Asp Ala Ile Gly Gly Val Ile Asn Ile Ile Thr Lys Pro
145             150                 155                 160

Val Asn Asn Gln Thr Trp Asp Gly Val Leu Gly Leu Gly Gly Ile Ile
            165                 170                 175

Gln Glu His Gly Lys Phe Gly Asn Ser Thr Thr Asn Asp Phe Tyr Leu
            180                 185                 190

Ser Gly Pro Leu Ile Lys Asp Lys Leu Gly Leu Gln Leu Tyr Gly Gly
        195                 200                 205

Met Asn Tyr Arg Lys Glu Asp Ser Ile Ser Gln Gly Thr Pro Ala Lys
    210                 215                 220

Asp Asn Lys Asn Ile Thr Ala Thr Leu Gln Phe Thr Pro Thr Glu Ser
225             230                 235                 240

Gln Lys Phe Val Phe Glu Tyr Gly Lys Asn Asn Gln Val His Thr Leu
                245                 250                 255

Thr Pro Gly Glu Ser Leu Asp Ala Trp Thr Met Arg Gly Asn Leu Lys
            260                 265                 270
```

```
Gln Pro Asn Ser Lys Arg Glu Thr His Asn Ser Arg Ser His Trp Val
        275                 280                 285

Ala Ala Trp Asn Ala Gln Gly Glu Ile Leu His Pro Glu Ile Ala Val
        290                 295                 300

Tyr Gln Glu Lys Val Ile Arg Glu Val Lys Ser Gly Lys Lys Asp Lys
305                 310                 315                 320

Tyr Asn His Trp Asp Leu Asn Tyr Glu Ser Arg Lys Pro Glu Ile Thr
                325                 330                 335

Asn Thr Ile Ile Asp Ala Lys Val Thr Ala Phe Leu Pro Glu Asn Val
                340                 345                 350

Leu Thr Ile Gly Gly Gln Phe Gln His Ala Glu Leu Arg Asp Asp Ser
        355                 360                 365

Ala Thr Gly Lys Lys Thr Thr Glu Thr Gln Ser Val Ser Ile Lys Gln
        370                 375                 380

Lys Ala Val Phe Ile Glu Asn Glu Tyr Ala Ala Thr Asp Ser Leu Ala
385                 390                 395                 400

Leu Thr Gly Gly Leu Arg Leu Asp Asn His Glu Ile Tyr Gly Ser Tyr
                405                 410                 415

Trp Asn Pro Arg Leu Tyr Ala Val Tyr Asn Leu Thr Asp Asn Leu Thr
                420                 425                 430

Leu Lys Gly Gly Ile Ala Lys Ala Phe Arg Ala Pro Ser Ile Arg Glu
        435                 440                 445

Val Ser Pro Gly Phe Gly Thr Leu Thr Gln Gly Gly Ala Ser Ile Met
        450                 455                 460

Tyr Gly Asn Arg Asp Leu Lys Pro Glu Thr Ser Val Thr Glu Glu Ile
465                 470                 475                 480

Gly Ile Ile Tyr Ser Asn Asp Ser Gly Phe Ser Ala Ser Ala Thr Leu
                485                 490                 495
```

Phe Asn Thr Asp Phe Lys Asn Lys Leu Thr Ser Tyr Asp Ile Gly Thr
            500   505   510

Lys Asp Pro Val Thr Gly Leu Asn Thr Phe Ile Tyr Asp Asn Val Gly
            515   520   525

Glu Ala Asn Ile Arg Gly Val Glu Leu Ala Thr Gln Ile Pro Val Tyr
    530   535   540

Asp Lys Trp His Val Ser Ala Asn Tyr Thr Phe Thr Asp Ser Arg Arg
545   550   555   560

Lys Ser Asp Asp Glu Ser Leu Asn Gly Lys Ser Leu Lys Gly Glu Pro
            565   570   575

Leu Glu Arg Thr Pro Arg His Ala Ala Asn Ala Lys Leu Glu Trp Asp
            580   585   590

Tyr Thr Gln Asp Ile Thr Phe Tyr Ser Ser Leu Asn Tyr Thr Gly Lys
            595   600   605

Gln Ile Trp Ala Ala Gln Arg Asn Gly Ala Lys Val Pro Arg Val Arg
    610   615   620

Asn Gly Phe Thr Ser Met Asp Ile Gly Leu Asn Tyr Gln Ile Leu Pro
625   630   635   640

Asp Thr Leu Ile Asn Phe Ala Val Leu Asn Val Thr Asp Arg Lys Ser
            645   650   655

Glu Asp Ile Asp Thr Ile Asp Gly Asn Trp Gln Val Asp Glu Gly Arg
            660   665   670

Arg Tyr Trp Ala Asn Val Arg Val Ser Phe
            675   680

<210> 41
<211> 164
<212> PRT
<213> Escherichia coli
<400> 41

Met Gly Phe Arg Lys Thr Ile Ile Thr Ser Val Gly Leu Ile Phe Ile
1   5   10.   15

```
Ser Phe Ser Phe Val Ala Lys Cys Ser Gln Leu Lys Asn Leu Asn Asn
            20                  25                  30

Tyr Ser Val Met Leu Cys Gly Lys Val Ser Asn Asn Ile Leu Asp Asp
            35                  40                  45

Ile Gly Gly Tyr Lys Glu Arg Asn Ile Leu Met Leu Arg Ala Ile Lys
        50                  55                  60

Lys Ile Ile Ile Met Thr Ile Val Asn Ile Ile Phe Phe Tyr Ser Phe
65              70                  75                  80

Gln Ser Thr Ala Asp Glu Met Val Leu Ile Lys Lys Tyr Gly Phe Gly
                85                  90                  95

Leu Glu Arg Asp Ile Lys Gly Arg Pro Leu Ile Tyr Pro Ile Glu Asn
            100                 105                 110

Tyr Asp Glu Cys Lys Lys Lys Cys Asn His Met Asn Tyr Ile Ala Asp
        115                 120                 125

Val Asn Ala Gln Leu Ala Met Ser Lys Lys Asn Asn Arg Ile Phe Ala
    130                 135                 140

Asn Ile Thr Phe Thr Asn Asn Ser Ser Thr Thr Tyr Phe Phe Leu Asn
145                 150                 155                 160

Ile Ile Tyr Leu


<210>    42
<211>    218
<212>    PRT
<213>    Escherichia coli
<400>    42

Met Asn Gln Ile Lys Asp Asn Lys Val Ile Met Lys Ile Lys Asn Leu
1               5                   10                  15

Ile Ser Val Ile Leu Leu Ser Gly Gly Ile Met Gly Thr Gly Leu Tyr
            20                  25                  30

Ser Ser Asp Asn His Gln Lys Ile Arg Ser Arg Phe Asn Ile Gln Glu
        35                  40                  45
```

```
Ser Tyr Cys Ala Ile Lys Thr Asn Gly Val Leu Gly Phe Ser Asn Arg
    50              55              60

Lys Asp Val Leu Arg Glu Asn Gly Asp Ser Thr Gly Thr Thr Ser Ser
65              70              75              80

Ser Thr Asn Ala Met Met Leu Met Glu Asn Gly Glu Asn Glu Ile Ser
                85              90              95

Leu Glu Ile Gly Ala Leu Arg Trp Phe Ser Asp Lys Pro Ala Ser Thr
            100             105             110

Glu Glu Arg Gly His Phe Ser Gln Lys Ala Gly Cys Ser Leu Asp Leu
            115             120             125

Val Arg Phe Val Lys Gln Glu Glu Thr Ile Leu Ser Ser Ile Lys Val
    130             135             140

Thr Ile Asn Gln Gln Gly Ile Pro Glu Ala Gln Pro Asp Ser Met His
145             150             155             160

Pro Val Ile Arg Lys Glu Ile Leu Ala Glu Gln Ala Glu Pro Gly Phe
            165             170             175

Ile Asp Pro Asp Tyr Phe Asn Glu Thr Tyr Phe Pro Lys Gly Met Lys
            180             185             190

Val Tyr Gln Phe Thr Gln Lys Val Ser Val Ala Gly Leu Pro Asp Gly
            195             200             205

Pro Gly Arg Ser Thr Pro Phe Thr Gly Ala
    210             215
```

```
<210>  43
<211>  2732
<212>  PRT
<213>  Escherichia coli
<400>  43
```

```
Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu
1               5               10              15

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala
```

```
            20                    25                    30

Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly
        35                    40                    45

Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His
    50                    55                    60

Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn
65                    70                    75                    80

Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln
                85                    90                    95

Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn
            100                   105                   110

Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val
        115                   120                   125

Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr
        130                   135                   140

Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr
145                   150                   155                   160

Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val
                165                   170                   175

Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg
                180                   185                   190

Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala
        195                   200                   205

Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr
        210                   215                   220

Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys
225                   230                   235                   240

Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile
                245                   250                   255
```

100

His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu
        260   265   270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr
        275   280   285

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly
    290   295   300

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser
305   310   315   320

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys
            325   330   335

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys
        340   345   350

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln
        355   360   365

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala
    370   375   380

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu
385   390   395   400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys
            405   410   415

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val
        420   425   430

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly
        435   440   445

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr
    450   455   460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser
465   470   475   480

Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Thr Met His Leu Val Leu
            485   490   495

Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys Gly
            500   505   510

Leu Thr Val Ser Ala Thr Ser Ser Gly Lys Lys Ser Val Thr His Ser
        515   520   525

Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu Asp Gly Glu
    530   535   540

Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys Leu Ser Thr
545   550   555   560

Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser Ile Asn Ala
        565   570   575

Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln Thr Met Val
        580   585   590

Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser Ser Ala Pro
      595   600   605

Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly Val Leu Val
    610   615   620

Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn Ser Gly Leu
625   630   635   640

Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg Leu Asp Asn
          645   650   655

Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr Leu Asp Ile
        660   665   670

Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn Gly Leu Met
      675   680   685

Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile Ala Asp Thr
    690   695   700

Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu Leu Gln Gly
705   710   715   720

Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln Gly Ser His
            725   730   735

Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly Lys Thr Leu
        740   745   750

Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val Gln Ala Asp
        755   760   765

Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn Leu Thr Ala
    770   775   780

Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met Ser Gln Gly
785   790   795   800

Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly Ser Leu Leu
            805   810   815

Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp Asn Arg Gly
        820   825   830

Thr Val Gln Gly Asn His Val Thr Ile Arg Gln Asn Ser Val Thr Asn
        835   840   845

Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala Ala Arg Met
    850   855   860

Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser Leu Leu Thr
865   870   875   880

Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser Ser Gly His
            885   890   895

Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu Ala Asn Ser
        900   905   910

Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu Thr Gly Glu
        915   920   925

Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly Glu Met Ala

```
        930                935                940

   Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile Ala Lys Asn
   945                950                955                960

   Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp Ile Thr Gly
                   965                970                975

   Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn Asn Gln Ala
                   980                985                990

   Asn Gly Lys Leu Leu Ser Ala Gly  Val Leu Thr Leu Lys  Ala Asp Ser
            995                1000                 1005

   Val Thr Asn Asp Gly Gln Leu  Gln Gly Asn Val Thr  Thr Ile Thr
       1010                1015                 1020

   Ala Gly Gln Leu Thr Asn Gly  Gly His Leu Gln Gly  Glu Thr Leu
       1025                1030                 1035

   Thr Leu Thr Ala Ser Gly Gly  Val Asn Asn Arg Ser  Gly Gly Val
       1040                1045                 1050

   Leu Met Ser Arg Asn Ala Leu  Asn Val Ser Thr Ala  Thr Leu Ser
       1055                1060                 1065

   Asn Gln Ser Thr Ile Gln Gly  Gly Gly Gly Val Ser  Leu Asn Ala
       1070                1075                 1080

   Thr Asp Arg Leu Gln Asn Asp  Gly Lys Ile Leu Ser  Gly Ser Asn
       1085                1090                 1095

   Leu Thr Leu Thr Ala Gln Val  Leu Ala Asn Thr Gly  Ser Gly Leu
       1100                1105                 1110

   Val Gln Ala Ala Thr Leu Leu  Leu Asp Val Val Asn  Thr Val Asn
       1115                1120                 1125

   Gly Gly Arg Val Leu Ala Thr  Gly Ser Asp Val Lys  Gly Thr Thr
       1130                1135                 1140

   Leu Asn Asn Thr Gly Thr Leu  Gln Gly Ala Thr Leu  Val Asn Tyr
       1145                1150                 1155
```

His Thr Phe Ser Ser Gly Thr Leu Leu Gly Thr Ser Gly Leu Gly
    1160   1165   1170

Val Lys Gly Ser Ser Leu Leu Gln Asn Gly Thr Gly Arg Leu Tyr
    1175   1180   1185

Ser Ala Gly Asn Leu Leu Leu Asp Ala Gln Asp Phe Ser Gly Gln
    1190   1195   1200

Gly Gln Val Val Ala Thr Gly Asp Val Thr Leu Lys Leu Ile Ala
    1205   1210   1215

Ala Leu Thr Asn His Gly Thr Leu Ala Ala Gly Lys Thr Leu Ser
    1220   1225   1230

Val Thr Ser Gln Asn Ala Ile Thr Asn Gly Gly Val Met Gln Gly
    1235   1240   1245

Asp Ala Met Val Leu Gly Ala Gly Glu Ala Phe Thr Asn Asn Gly
    1250   1255   1260

Leu Thr Ala Gly Lys Gly Asn Ser Val Phe Ser Ala Gln Arg Leu
    1265   1270   1275

Phe Leu Asn Ala Pro Gly Ser Leu Gln Gly Gly Gly Asp Val Ser
    1280   1285   1290

Leu Asn Ser Arg Ser Asp Ile Thr Ile Ser Gly Phe Thr Gly Thr
    1295   1300   1305

Ala Gly Ser Leu Thr Met Asn Val Ala Gly Thr Leu Leu Asn Ser
    1310   1315   1320

Ala Leu Ile Tyr Ala Gly Asn Asn Leu Lys Leu Phe Thr Asp Arg
    1325   1330   1335

Leu His Asn Gln His Gly Asp Ile Leu Ala Gly Asn Ser Leu Trp
    1340   1345   1350

Val Gln Lys Asp Ala Ser Gly Gly Ala Asn Thr Glu Ile Ile Asn
    1355   1360   1365

Asn Ser Gly Asn Ile Glu Thr His Gln Gly Asp Ile Val Val Arg
    1370   1375   1380

Thr Gly His Leu Leu Asn Gln Arg Glu Gly Phe Ser Ala Thr Thr
    1385   1390   1395

Thr Thr Arg Thr Asn Pro Ser Ser Ile Gln Gly Met Gly Asn Ala
    1400   1405   1410

Leu Val Asp Ile Pro Leu Ser Leu Leu Pro Asp Gly Ser Tyr Gly
    1415   1420   1425

Tyr Phe Thr Arg Glu Val Glu Asn Gln His Gly Thr Pro Cys Asn
    1430   1435   1440

Gly His Gly Ala Cys Asn Ile Thr Met Asp Thr Leu Tyr Tyr Tyr
    1445   1450   1455

Ala Pro Phe Ala Asp Ser Ala Thr Gln Arg Phe Leu Ser Ser Gln
    1460   1465   1470

Asn Ile Thr Thr Val Thr Gly Ala Asp Asn Pro Ala Gly Arg Ile
    1475   1480   1485

Ala Ser Gly Arg Asn Leu Ser Ala Glu Ala Glu Arg Leu Glu Asn
    1490   1495   1500

Arg Ala Ser Phe Ile Leu Ala Asn Gly Asp Ile Ala Leu Ser Gly
    1505   1510   1515

Arg Glu Leu Ser Asn Gln Ser Trp Gln Thr Gly Thr Glu Asn Glu
    1520   1525   1530

Tyr Leu Val Tyr Arg Tyr Asp Pro Lys Thr Phe Tyr Gly Ser Tyr
    1535   1540   1545

Ala Thr Gly Ser Leu Asp Lys Leu Pro Leu Leu Ser Pro Glu Phe
    1550   1555   1560

Glu Asn Asn Thr Ile Arg Phe Ser Leu Asp Gly Arg Glu Lys Asp
    1565   1570   1575

```
Tyr Thr  Pro Gly Lys Thr Tyr  Tyr Ser Val Ile Gln  Ala Gly Gly
    1580                 1585              1590

Asp Val  Lys Thr Arg Phe Thr  Ser Ser Ile Asn Asn  Gly Thr Thr
    1595                 1600              1605

Thr Ala  His Ala Gly Ser Val  Ser Pro Val Val Ser  Ala Pro Val
    1610                 1615              1620

Leu Asn  Thr Leu Ser Gln Gln  Thr Gly Gly Asp Ser  Leu Thr Gln
    1625                 1630              1635

Thr Ala  Leu Gln Gln Tyr Glu  Pro Val Val Val Gly  Ser Pro Gln
    1640                 1645              1650

Trp His  Asp Glu Leu Ala Gly  Ala Leu Lys Asn Ile  Ala Gly Gly
    1655                 1660              1665

Ser Pro  Leu Thr Gly Gln Thr  Gly Ile Ser Asp Asp  Trp Pro Leu
    1670                 1675              1680

Pro Ser  Gly Asn Asn Gly Tyr  Leu Val Pro Ser Thr  Asp Pro Asp
    1685                 1690              1695

Ser Pro  Tyr Leu Ile Thr Val  Asn Pro Lys Leu Asp  Gly Leu Gly
    1700                 1705              1710

Gln Val  Asp Ser His Leu Phe  Ala Gly Leu Tyr Glu  Leu Leu Gly
    1715                 1720              1725

Ala Lys  Pro Gly Gln Ala Pro  Arg Glu Thr Ala Pro  Ser Tyr Thr
    1730                 1735              1740

Asp Glu  Lys Gln Phe Leu Gly  Ser Ser Tyr Phe Leu  Asp Arg Leu
    1745                 1750              1755

Gly Leu  Lys Pro Glu Lys Asp  Tyr Arg Phe Leu Gly  Asp Ala Val
    1760                 1765              1770

Phe Asp  Thr Arg Tyr Val Ser  Asn Ala Val Leu Ser  Arg Thr Gly
    1775                 1780              1785

Ser Arg  Tyr Leu Asn Gly Leu  Gly Ser Asp Thr Glu  Gln Met Arg
```

```
            1790                    1795                    1800


     Tyr Leu Met Asp Asn Ala Ala  Arg Gln Gln Lys Gly  Leu Gly Leu
         1805                1810              1815


     Glu Phe Gly Val Ala Leu Thr  Ala Glu Gln Ile Ala  Gln Leu Asp
         1820                1825              1830


     Gly Ser Ile Leu Trp Trp Glu  Ser Val Thr Ile Asn  Gly Gln Thr
         1835                1840              1845


     Val Met Val Pro Lys Leu Tyr  Leu Ser Pro Glu Asp  Ile Thr Leu
         1850                1855              1860


     His Asn Gly Ser Val Ile Ser  Gly Asn Asn Val Gln  Leu Ala Gly
         1865                1870              1875


     Gly Asn Ile Thr Asn Ser Gly  Gly Ser Ile Asn Ala  Gln Asn Asp
         1880                1885              1890


     Leu Ser Leu Asp Ser Ser Gly  Tyr Ile Asp Asn Leu  Asn Ala Gly
         1895                1900              1905


     Leu Ile Ser Ala Gly Gly Ser  Leu Asp Leu Ser Ala  Ile Gly Asp
         1910                1915              1920


     Ile Ser Asn Ile Ser Ser Val  Ile Ser Gly Lys Thr  Val Gln Leu
         1925                1930              1935


     Glu Ser Val Ser Gly Asn Ile  Ser Asn Ile Thr Arg  Arg Gln Gln
         1940                1945              1950


     Trp Asn Ala Gly Ser Asp Ser  Gln Tyr Gly Gly Val  His Leu Ser
         1955                1960              1965


     Gly Thr Asp Thr Gly Pro Val  Ala Thr Ile Lys Gly  Thr Asp Ser
         1970                1975              1980


     Leu Ser Leu Asp Ala Gly Lys  Asn Ile Asp Ile Thr  Gly Ala Thr
         1985                1990              1995


     Val Ser Ser Gly Gly Asp Leu  Gly Met Ser Ala Gly  Asn Asp Ile
         2000                2005              2010
```

```
Asn Ile  Ala Ala Asn Leu Ile  Ser Gly Ser Lys Ser  Gln Ser Gly
    2015             2020             2025

Phe Trp  His Thr Asp Asp Asn  Ser Ser Ser Ser Thr  Thr Ser Gln
    2030             2035             2040

Gly Ser  Ser Ile Ser Ala Gly  Gly Asn Leu Ala Met  Ala Ala Gly
    2045             2050             2055

His Asn  Leu Asp Val Thr Ala  Ser Ser Val Ser Ala  Gly His Ser
    2060             2065             2070

Ala Leu  Leu Ser Cys Arg Ser  Arg Pro Ser Leu Glu  Cys Ser Gln
    2075             2080             2085

Gly Lys  Ala Lys Thr Ser Arg  Asn Gly Arg Ser Glu  Ser His Glu
    2090             2095             2100

Ser His  Ala Ala Val Ser Thr  Val Thr Ala Gly Asp  Asn Phe Leu
    2105             2110             2115

Leu Val  Ala Gly Arg Asp Ile  Ala Ser Gln Ala Ala  Gly Met Ala
    2120             2125             2130

Ala Glu  Asn Asn Val Val Ile  Arg Gly Gly Arg Asp  Val Asn Leu
    2135             2140             2145

Val Ala  Glu Ser Ala Gly Ala  Gly Asp Ser Tyr Thr  Ser Lys Lys
    2150             2155             2160

Lys Lys  Glu Ile Asn Glu Thr  Val Arg Gln Gln Gly  Thr Glu Ile
    2165             2170             2175

Ala Ser  Gly Gly Asp Thr Thr  Val Asn Ala Gly Arg  Asp Ile Thr
    2180             2185             2190

Ala Val  Ala Ser Ser Val Thr  Ala Thr Gly Asn Ile  Ser Val Asn
    2195             2200             2205

Ala Gly  Arg Asp Val Ala Leu  Thr Thr Ala Thr Glu  Ser Asp Tyr
    2210             2215             2220
```

His Tyr Leu Glu Thr Lys Lys Lys Ser Gly Gly Phe Leu Ser Lys
    2225   2230   2235

Lys Thr Thr Arg Thr Ile Ser Glu Asp Ser Ala Thr Arg Glu Ala
    2240   2245   2250

Gly Ser Leu Leu Ser Gly Asn Arg Val Thr Val Asn Ala Gly Asp
    2255   2260   2265

Asn Leu Thr Val Glu Gly Ser Asp Val Val Ala Asp Arg Asp Val
    2270   2275   2280

Ser Leu Ala Ala Gly Asn His Val Asp Val Leu Ala Ala Thr Ser
    2285   2290   2295

Thr Asp Thr Ser Trp Arg Phe Lys Glu Thr Lys Lys Ser Gly Leu
    2300   . 2305   2310

Met Gly Thr Gly Gly Ile Gly Phe Thr Ile Gly Ser Ser Lys Thr
    2315   2320   2325

Thr His Asp Arg Arg Glu Ala Gly Thr Thr Gln Ser Gln Ser Ala
    2330   2335   2340

Ser Thr Ile Gly Ser Thr Ala Gly Asn Val Ser Ile Thr Ala Gly
    2345   2350   2355

Lys Gln Ala His Ile Ser Gly Ser Asp Val Ile Ala Asn Arg Asp
    2360   2365   2370

Ile Ser Ile Thr Gly Asp Ser Val Val Val Asp Pro Gly His Asp
    2375   2380   2385

Arg Arg Thr Val Asp Glu Lys Phe Glu Gln Lys Lys Ser Gly Leu
    2390   2395   2400

Thr Val Ala Leu Ser Gly Thr Val Gly Ser Ala Ile Asn Asn Ala
    2405   2410   2415

Val Thr Ser Ala Gln Glu Thr Lys Glu Ser Ser Asp Ser Arg Leu
    2420   2425   2430

```
Lys Ala  Leu Gln Ala Thr Lys  Thr Ala Leu Ser Gly  Val Gln Ala
    2435              2440                   2445

Gly Gln  Ala Ala Thr Met Ala  Ser Ala Thr Gly Asp  Pro Asn Ala
    2450              2455                   2460

Gly Val  Ser Leu Ser Leu Thr  Thr Gln Lys Ser Lys  Ser Gln Gln
    2465              2470                   2475

His Ser  Glu Ser Asp Thr Val  Ser Gly Ser Thr Leu  Asn Ala Gly
    2480              2485                   2490

Asn Asn  Leu Ser Val Val Ala  Thr Gly Lys Asn Arg  Gly Asp Asn
    2495              2500                   2505

Arg Gly  Asp Ile Val Ile Ala  Gly Ser Gln Leu Lys  Ala Gly Gly
    2510              2515                   2520

Asn Thr  Ser Leu Asp Ala Ala  Asn Asp Ile Leu Leu  Ser Gly Ala
    2525              2530                   2535

Ala Asn  Thr Gln Lys Thr Thr  Gly Arg Asn Ser Ser  Ser Gly Gly
    2540              2545                   2550

Gly Val  Gly Val Ser Ile Gly  Ala Gly Lys Gly Ala  Gly Ile Ser
    2555              2560                   2565

Ala Phe  Ala Ser Val Asn Ala  Ala Lys Gly Arg Glu  Lys Gly Asn
    2570              2575                   2580

Gly Thr  Thr Thr Asp Lys Thr  Val Thr Ile Asn Ser  Gly Arg Asp
    2585              2590                   2595

Thr Val  Leu Asn Gly Ala Gln  Val Asn Gly Asn Arg  Ile Ile Ala
    2600              2605                   2610

Asp Val  Gly His Asp Leu Leu  Ile Ser Ser Gln Gln  Asp Thr Ser
    2615              2620                   2625

Lys Tyr  Asp Ser Lys Gln Thr  Ser Val Ala Ala Gly  Gly Ser Phe
    2630              2635                   2640

Thr Phe  Gly Ser Met Thr Gly  Ser Gly Tyr Ile Ala  Ala Ser Arg
```

```
              2645                    2650                    2655


    Asp Lys  Met Lys Ser Arg  Phe  Asp Ser Val Ala  Glu  Gln Thr Gly
        2660                    2665                    2670


    Met Phe  Ala Arg Val Met  Val  Ala Ser Thr Ser  Gln  Trp Val Asn
        2675                    2680                    2685


    Ile Pro  Asn Trp Met Val  Arg  Ser Leu Pro His  Cys  His Thr Gly
        2690                    2695                    2700


    Glu Lys  Pro Pro Gly Tyr  Arg  Thr Leu Gly Leu  Val  Thr Leu Gln
        2705                    2710                    2715


    Arg Ser  Gly Ile Ile Lys  Ser  Ser His Arg Trp  Asn  Gln Ser
        2720                    2725                    2730
```

<210> 44
<211> 321
<212> PRT
<213> Escherichia coli
<400> 44

```
    Met Met Leu Lys Lys Thr Ile Phe Ile Leu Thr Leu Phe Ser Gly Asn
    1                   5                   10                  15


    Val Ile Ala Ala Thr Val Glu Leu Gly Phe Glu Asn Glu Gln Tyr Asn
                    20                  25                  30


    Tyr Ala Tyr Arg Ser Ala Asp Val Phe Met Pro Tyr Ile Lys Ser Asn
                35                  40                  45


    Phe Asn Pro Val Thr Asp Ser Ala Leu Asn Val Ser Leu Thr Tyr Met
        50                  55                  60


    Tyr Gln Asp Gln Tyr Gly Lys Lys His Lys Lys Thr Ser Glu Asp Arg
    65                  70                  75                  80


    Phe Lys Thr Asn Arg Asp Arg Ile Glu Leu Tyr Leu Lys Gly Tyr Thr
                    85                  90                  95


    Leu Asn Arg Gly Ala Tyr Ser Phe Ser Pro Ser Ala Gly Phe Arg Tyr
                    100                 105                 110
```

Glu Ser Trp Asp Val Asn Tyr Asp Asn Pro Lys Lys Gln Asp Lys Trp
        115   120   125

Lys Leu Glu Leu Arg Phe Tyr Pro Asn Met Thr Tyr Lys Leu Asn Asp
        130   135   140

Gln Leu Ser Leu Tyr Met Asn Gly Phe Val Ala Pro Val Phe Phe Lys
145   150   155   160

Thr Gln Gln Glu Ser Arg Lys Asp Asn Asn Tyr Val Lys Gly Lys Leu
            165   170   175

Gly Ala Lys Arg Tyr Asn Asn Asp Tyr Tyr Gln Glu Leu Gln Ile Leu
            180   185   190

Gly Val Arg Tyr Lys Phe Asn Asn Asp Asn Thr Leu Trp Ala Ser Val
        195   200   205

Tyr Asn Glu Arg Lys Tyr Asn Gln His Ser Ser Lys Tyr Asp Arg Trp
    210   215   220

Gln Leu Arg Gly Gly Tyr Asp Phe Lys Val Thr Glu Glu Phe Val Leu
225   230   235   240

Ser Pro Phe Ile Arg Tyr Asp Leu Ser Tyr Arg Glu Lys Asn Leu Glu
            245   250   255

Ser Thr Ser Asn Asn Gly Leu Ser Lys Asn Asn Lys Glu Ile Arg Thr
            260   265   270

Gly Ala Ser Phe Ser Tyr Lys Ile Ile Pro Ser Val Lys Leu Val Gly
        275   280   285

Glu Ile Tyr Arg Gln Thr Thr Asn Ile Glu Asn Tyr Tyr Gly Glu His
    290   295   300

Ser Glu Asp Lys Asn Arg Met Phe Tyr Lys Leu Gly Ile Asn Lys Thr
305   310   315   320

Phe

<210>   45

<211> 587
<212> PRT
<213> Escherichia coli
<400> 45

Met Gln His Arg Gln Lys Asn Ile Leu Thr Lys Thr Ser Leu Leu Ser
1   5   10   15

Arg Ala Leu Ser Val Pro Cys Cys Asp Met Phe Arg Arg Gly Ser Pro
            20   25   30

Trp Ile Cys Tyr Leu Ser Leu Ser Val Phe Ser Gly Cys Phe Ile Pro
        35   40   45

Ala Phe Ser Ser Pro Ala Ala Met Leu Ser Pro Gly Asp Arg Ser Ala
    50   55   60

Ile Gln Gln Gln Gln Gln Gln Leu Leu Asp Glu Asn Gln Arg Gln Arg
65   70   75   80

Asp Ala Leu Glu Arg Pro Leu Thr Ile Thr Pro Ser Pro Glu Thr Ser
            85   90   95

Ala Gly Thr Glu Gly Pro Cys Phe Thr Val Ser Ser Ile Val Val Ser
            100   105   110

Gly Ala Thr Arg Leu Thr Ser Ala Glu Thr Asp Arg Leu Val Pro Trp
        115   120   125

Val Asn Gln Cys Leu Asn Ile Thr Gly Leu Thr Ala Val Thr Asp Ala
    130   135   140

Val Thr Asp Gly Tyr Ile Arg Arg Gly Tyr Ile Thr Ser Arg Ala Phe
145   150   155   160

Leu Thr Glu Gln Asp Leu Ser Gly Gly Val Leu His Ile Thr Val Met
                165   170   175

Glu Gly Arg Leu Gln Gln Ile Arg Ala Glu Gly Ala Asp Leu Pro Ala
            180   185   190

Arg Thr Leu Lys Met Val Phe Pro Gly Met Glu Gly Lys Val Leu Asn
        195   200   205

114

```
Leu Arg Asp Ile Glu Gln Gly Met Glu Gln Ile Asn Arg Leu Arg Thr
    210             215             220

Glu Pro Val Gln Ile Glu Ile Ser Pro Gly Asp Arg Glu Gly Trp Ser
225             230             235             240

Val Val Thr Leu Thr Ala Leu Pro Glu Trp Pro Val Thr Gly Ser Val
            245             250             255

Gly Ile Asp Asn Ser Gly Gln Lys Ser Thr Gly Thr Gly Gln Leu Asn
            260             265             270

Gly Val Leu Ser Phe Asn Asn Pro Leu Gly Leu Ala Asp Asn Trp Phe
            275             280             285

Val Ser Gly Gly Arg Ser Ser Asp Phe Ser Val Ser His Asp Ala Arg
    290             295             300

Asn Phe Ala Ala Gly Val Ser Leu Pro Tyr Gly Tyr Thr Leu Val Asp
305             310             315             320

Tyr Thr Tyr Ser Trp Ser Asp Tyr Leu Ser Thr Ile Asp Asn Arg Gly
            325             330             335

Trp Arg Trp Arg Ser Thr Gly Asp Leu Gln Thr His Arg Leu Gly Leu
            340             345             350

Ser His Val Leu Phe Arg Asn Gly Asp Met Lys Thr Ala Leu Thr Gly
            355             360             365

Gly Leu Gln His Arg Ile Ile His Asn Tyr Leu Asp Asp Val Leu Leu
    370             375             380

Gln Gly Ser Ser Arg Lys Leu Thr Ser Phe Ser Val Gly Leu Asn His
385             390             395             400

Thr His Lys Phe Leu Gly Gly Val Gly Thr Leu Asn Pro Val Phe Thr
            405             410             415

Arg Gly Met Pro Trp Phe Gly Ala Glu Ser Asp His Gly Lys Arg Gly
            420             425             430

Asp Leu Pro Val Asn Gln Phe Arg Lys Trp Ser Val Ser Ala Ser Phe
```

```
              435                    440                    445

    Gln Arg Pro Val Thr Asp Arg Val Trp Trp Leu Thr Ser Ala Tyr Ala
        450                   455                   460

    Gln Trp Ser Pro Asp Arg Leu His Gly Val Glu Gln Leu Ser Leu Gly
    465                   470                   475                   480

    Gly Glu Ser Ser Val Arg Gly Phe Lys Asp Gln Tyr Ile Ser Gly Asn
                  485.                  490                   495

    Asn Gly Gly Tyr Leu Arg Asn Glu Leu Ser Trp Ser Leu Phe Ser Leu
                  500                   505                   510

    Pro Tyr Val Gly Thr Val Arg Ala Val Ala Ala Leu Asp Gly Gly Trp
                  515                   520                   525

    Leu His Ser Asp Ser Asp Asp Pro Tyr Ser Ser Gly Thr Leu Trp Gly
        530                   535                   540

    Ala Ala Ala Gly Leu Ser Thr Thr Ser Gly His Val Ser Gly Ser Phe
    545                   550                   555                   560

    Thr Ala Gly Leu Pro Leu Val Tyr Pro Asp Trp Leu Ala Pro Asp His
                  565                   570                   575

    Leu Thr Val Tyr Trp Arg Val Ala Val Ala Phe
                  580                   585
```

<210> 46
<211> 744
<212> PRT
<213> Escherichia coli
<400> 46

```
    Met Asn Lys His Thr Leu Leu Leu Thr Val Leu Phe Leu Asn Leu Ile
    1               5                   10                  15

    Cys Thr Pro Val Phe Ala Gln Asn Trp Gln Val Ala Thr Phe Gly Gln
                  20                  25                  30

    Ser Thr Asp Leu Asn Phe Ser Ser Leu Ile Asp Ser Ala Lys Ile Gly
                  35                  40                  45
```

Arg Asn Asn Ala Trp Leu Ala Gly Asn Asn Asn Phe Leu Glu Ala Gly
    50   55   60

Lys Phe Tyr Thr Leu Pro Thr Asp Phe Phe Ile Glu Ser Arg Gly Gly
65   70   75   80

Lys Ile Ala Asn Ser His Asp Gly Met Thr Val Phe Tyr Thr Ile Val
            85   90   95

Pro Val Thr Gln Thr Phe Arg Leu Glu Ala Asp Leu Thr Leu Glu Gln
            100   105   110

Ile Gly Pro Glu Val Asn Gly Lys Ser Pro Ala Gly Gln Glu Gly Ala
        115   120   125

Gly Leu Phe Val Arg Asp Ile Ile Gly Pro Gln Arg Gln Glu Pro Gln
    130   135   140

Ser Ala Gly Thr Glu Glu Tyr Pro Gln Ala Ser Asn Ile Leu Met Asn
145   150   155   160

Ala Phe Ile Thr Gln Asn Lys Lys Asn Asp Asn Leu Val Gln Ile Thr
            165   170   175

Ser Ile Val Arg Glu Gly Val Ile Lys Thr Trp Gly Asn Glu Gly Ile
        180   185   190

Thr Ile Lys Lys Gln Pro Ile Ile Glu Asn Ile Asn Phe Thr Gln Lys
        195   200   205

Arg Asn Ile His Met Thr Ile Glu Arg Leu Pro Glu Lys Phe Ile Leu
    210   215   220

Thr Ala Phe Asp Thr Asp Arg Lys Glu Asn Gln Ser Trp Gln Phe Ser
225   230   235   240

Asp Tyr Ser Gly Phe Met Asn Gln Leu Asp Asn Asn Ser Leu Ala Ile
            245   250   255

Gly Phe Phe Ala Ala Arg Asn Ala Lys Leu Arg Val Lys Asn Ala Ser
            260   265   270

Phe Lys Pro Gly Lys Pro Leu Val Asp Tyr Lys Gln Leu Thr Ser Arg

```
            275                    280                    285

Gln Phe Ser Arg Val Arg His Lys Ala Pro Glu Leu Phe Leu Ala Ser
    290                    295                    300

Pro Gln Ser Val Val Arg Asn Ser Thr Thr Leu Gln Phe Leu Ala Asn
305                    310                    315                    320

Gln Ala Gly Ile Val Ser Ile Asp Asn Asp Lys Gln Thr Lys Gln Val
                325                    330                    335

Gln Ala Gly Glu Leu Val Gln Phe Pro Val Thr Leu Gln Lys Lys His
            340                    345                    350

Asn Asp Phe Thr Val Asn Phe Asn Val Asp Gly Asn Ile Ser Lys Lys
            355                    360                    365

Ala Ile Arg Ile Glu Gln Val Lys Ser Asn Leu Thr Asp Pro Tyr Glu
    370                    375                    380

Ile Tyr Val Cys Ser Asp Cys Arg Gln Gly Ala Arg Gly Ser Lys Asn
385                    390                    395                    400

Asp Pro Val Asp Leu Gln Thr Ala Val Lys Phe Val Ala Pro Gly Gly
            405                    410                    415

Asn Ile Tyr Leu Asn Asp Gly Gln Tyr His Gly Ile Thr Leu Asp Arg
            420                    425                    430

Glu Leu Ser Gly Ile Pro Gly Lys Tyr Lys Thr Ile Ser Ala Ile Asn
            435                    440                    445

Pro His Lys Ala Ile Phe Ile Asn Lys Thr Phe Asn Leu Asp Ala Ser
    450                    455                    460

Tyr Trp His Leu Lys Ser Val Val Phe Asp Gly Asn Val Asp Asn Gly
465                    470                    475                    480

Asn Asn Lys Pro Ala Tyr Leu Arg Ile Ala Gly Ser Tyr Asn Ile Ile
            485                    490                    495

Glu His Val Ile Ala Arg Asn Asn Asp Asp Thr Gly Ile Ser Ile Ser
            500                    505                    510
```

```
Ala Lys Asp Lys Asn Arg Phe Phe Trp Pro Ala His Asn Leu Val Leu
    515                 520             525

Asn Ser Asp Ser Tyr Asn Asn Leu Asp Leu Ser Gly Ile Asn Ala Asp
    530                 535             540

Gly Phe Ala Ala Lys Leu Gly Val Gly Pro Gly Asn Ile Phe Arg Gly
545                 550             555                 560

Cys Ile Ala His Asn Asn Ala Asp Asp Gly Trp Asp Leu Phe Asn Lys
            565             570                 575

Ile Glu Asp Gly Pro Asn Ala Ser Val Thr Ile Glu Asn Ser Val Ala
            580             585                 590

Tyr Glu Asn Gly Leu Pro Tyr Asn Lys Ala Asp Ile Leu Lys Gly Ser
    595                 600             605

Ile Gly Asn Gly Gly Glu Gly Gln Pro Ser Lys Ser Gln Val Ile Asn
    610                 615             620

Ser Ile Ala Ile Asn Asn Asn Met Asp Gly Phe Thr Asp Asn Phe Asn
625                 630             635                 640

Thr Gly Ser Leu Ile Val Arg Asn Asn Ile Ala Met Asn Asn Ala Arg
                645             650                 655

Tyr Asn Tyr Ile Leu Arg Thr Asn Pro Tyr Lys Phe Pro Ser Ser Ile
            660             665                 670

Leu Phe Asp Asn Asn Tyr Ser Ile Arg Asp Asp Trp Glu Asn Lys Ile
        675             680             685

Lys Asp Phe Leu Gly Asp Thr Val Asn Ser Val Asn Tyr Lys Leu Leu
    690                 695             700

Val Ser His Glu Thr Gly Pro Val Gln Lys Asp Leu Phe Phe Thr Arg
705                 710             715                 720

Asp Asp Ser Gly Asn Ile Ile Tyr Pro Asp Phe Phe Leu Asn Ile Ile
                725             730                 735
```

```
Asn Lys Phe Asn Glx Thr Met Pro
            740


<210>  47
<211>  136
<212>  PRT
<213>  Escherichia coli
<400>  47

Met Lys Thr Phe Ile Lys Thr Leu Leu Val Ala Val Thr Ile Leu Phe
1               5               10              15


Ser Val Phe Ala Thr Ala Lys Gln Val Lys Leu Pro Asn Asn Ile Lys
            20              25              30


Tyr Val Asn Thr Thr Glu Ala Phe Ser Cys Thr Glu Ile Asp Gly Met
        35              40              45


Asn Cys Gln Thr Lys Asn Pro Phe Asn Tyr Lys Asp Asn Ser Tyr Val
    50              55              60


Phe Val Leu Glu Arg Gly Gly Ala Trp Cys Tyr Asp Tyr Thr Val Ser
65              70              75              80


Val Leu Asn Leu Lys Thr Gly Lys Ala Gln Met Leu Glu Tyr Lys Asp
            85              90              95


Asn Gln Leu Cys Ser Gly Ser Asn Lys Pro Phe Phe Glu Ile Lys Asn
            100             105             110


Gly Val Pro Thr Val Gly Val Ile Asp Thr Ser Gly Lys Pro Val Val
        115             120             125


Val Ala Leu Asp Lys Leu Lys Thr
    130             135


<210>  48
<211>  225
<212>  PRT
<213>  Escherichia coli
<400>  48

Met Gln Leu Pro Val Lys Leu Leu Met Ser Leu Ile Ser Leu Val Ser
1               5               10              15
```

```
Val Ile Ala Arg Ala Gly Lys Tyr Lys Asn Tyr Ile Arg Asp Glu Ile
            20              25              30

Lys Tyr Trp Arg Tyr Thr Ser Tyr Lys Gly Gly Glu Phe Pro Glu Gly
            35              40              45

Phe Thr Asp Glu Lys Phe Ser Ser Ala Ile Tyr Asn Gly Arg Ile Phe
        50              55              60

Thr Met Lys Arg Leu His Thr Leu Met Leu Phe Leu Ala Val Leu Phe
65              70              75              80

Thr Gly Phe Asn Val Glu Ala Ala Ser Val Lys Gln Ala Leu Ser Cys
                85              90              95

Asp Pro Asn Ala Arg Ala Glu Gln Pro Gly Ala Cys Pro Thr Thr Tyr
            100             105             110

Glu Leu Tyr Glu Gly Asp Ala Ala Tyr Lys Ala Ala Leu Asp Lys Ala
        115             120             125

Leu Lys Pro Val Gly Leu Ser Gly Met Phe Gly Lys Gly Gly Tyr Met
    130             135             140

Asp Gly Pro Gly Gly Asn Val Thr Pro Val Thr Ile Asn Gly Thr Val
145             150             155             160

Trp Leu Gln Gly Asp Gly Cys Lys Ala Asn Thr Cys Gly Trp Asp Phe
            165             170             175

Ile Val Thr Leu Tyr Asn Pro Lys Thr His Glu Val Val Gly Tyr Arg
            180             185             190

Tyr Phe Gly Leu Asp Asp Pro Ala Tyr Leu Val Trp Phe Gly Glu Ile
        195             200             205

Gly Val His Glu Phe Ala Tyr Leu Val Lys Asn Tyr Val Ala Ala Val
    210             215             220

Asn
225


<210>   49
```

```
<211>   721
<212>   PRT
<213>   Escherichia coli
<400>   49
```

Met Lys Thr Gln Ile Thr Phe Ala Ala Leu Leu Pro Ala Leu Ala Ser
1   5   10   15

Phe Ile Pro Leu His Ala His Ala Ser Ser Thr Ser Glu Asp Glu Met
            20   25   30

Ile Val Thr Gly Asn Thr Ala Ala Asp Thr Thr Asp Ser Ala Ala Gly
        35   40   45

Ala Gly Phe Lys Thr Asn Asp Ile Asp Val Gly Pro Leu Gly Thr Lys
    50   55   60

Ser Trp Ile Glu Thr Pro Tyr Ser Ser Thr Thr Val Thr Lys Glu Met
65   70   75   80

Ile Glu Asn Gln Gln Ala Gln Ser Val Ser Glu Met Leu Lys Tyr Ser
            85   90   95

Pro Ser Thr Gln Met Gln Ala Arg Gly Gly Met Asp Val Gly Arg Pro
            100   105   110

Gln Ser Arg Gly Met Gln Gly Ser Val Val Ala Asn Ser Arg Leu Asp
        115   120   125

Gly Leu Asn Ile Val Ser Thr Thr Ala Phe Pro Val Glu Met Leu Glu
    130   135   140

Arg Met Asp Val Leu Asn Ser Leu Thr Gly Ala Leu Tyr Gly Pro Ala
145   150   155   160

Ser Pro Ala Gly Gln Phe Asn Phe Val Ala Lys Arg Pro Thr Glu Glu
            165   170   175

Thr Leu Arg Lys Val Thr Leu Gly Tyr Gln Ser Arg Ser Ala Phe Thr
            180   185   190

Gly His Ala Asp Leu Gly Gly His Phe Asp Glu Asn Lys Arg Phe Gly
        195   200   205

Tyr Arg Val Asn Leu Leu Asp Gln Glu Gly Glu Gly Asn Val Asp Asp
    210   215   220

Ser Thr Leu Arg Arg Lys Leu Val Ser Val Ala Leu Asp Trp Asn Ile
225   230   235   240

Gln Pro Gly Thr Gln Leu Gln Leu Asp Ala Ser His Tyr Glu Phe Ile
                245   250   255

Gln Lys Gly Tyr Val Gly Ser Phe Asn Tyr Gly Pro Asn Val Lys Leu
                260   265   270

Pro Ser Ala Pro Asn Pro Lys Asp Lys Asn Leu Ala Leu Ser Thr Ala
        275   280   285

Gly Asn Asp Leu Thr Thr Asp Thr Ile Ser Thr Arg Leu Ile His Tyr
    290   295   300

Phe Asn Asp Asp Trp Ser Met Asn Ala Gly Val Gly Trp Gln Gln Ala
305   310   315   320

Asp Arg Ala Met Arg Ser Val Ser Ser Lys Ile Leu Asn Asn Gln Gly
            325   330   335

Asp Ile Ser Arg Ser Met Lys Asp Ser Thr Ala Ala Gly Arg Phe Arg
            340   345   350

Val Leu Ser Asn Thr Ala Gly Leu Asn Gly His Ile Asp Thr Gly Ser
    355   360   365

Ile Gly His Asp Leu Ser Leu Ser Thr Thr Gly Tyr Val Trp Ser Leu
    370   375   380

Tyr Ser Ala Lys Gly Thr Gly Ser Ser Tyr Ser Trp Gly Thr Thr Asn
385   390   395   400

Met Tyr His Pro Asp Ala Ile Asp Glu Gln Gly Asp Gly Lys Ile Arg
            405   410   415

Thr Gly Gly Pro Arg Tyr Arg Ser Ser Val Asn Thr Gln Gln Ser Val
            420   425   430

Thr Leu Gly Asp Thr Val Thr Phe Thr Pro Gln Trp Ser Ala Met Phe

```
              435                    440                    445

Tyr Leu Ser Gln Ser Trp Leu Gln Thr Lys Asn Tyr Asp Lys His Gly
    450             455             460

Asn Gln Thr Asn Gln Val Asp Glu Asn Gly Leu Ser Pro Asn Ala Ala
465             470             475             480

Leu Met Tyr Lys Ile Thr Pro Asn Thr Met Ala Tyr Val Ser Tyr Ala
            485             490             495

Asp Ser Leu Glu Gln Gly Gly Thr Ala Pro Thr Asp Glu Ser Val Lys
            500             505             510

Asn Ala Gly Gln Thr Leu Asn Pro Tyr Arg Ser Lys Gln Tyr Glu Val
            515             520             525

Gly Leu Lys Ser Asp Ile Gly Glu Met Asn Leu Gly Ala Ala Leu Phe
    530             535             540

Arg Leu Glu Arg Pro Phe Ala Tyr Leu Asp Thr Asp Asn Val Tyr Lys
545             550             555             560

Glu Gln Gly Asn Gln Val Asn Asn Gly Leu Glu Leu Thr Ala Ala Gly
            565             570             575

Asn Val Trp Gln Gly Leu Asn Ile Tyr Ser Gly Val Thr Phe Leu Asp
            580             585             590

Pro Lys Leu Lys Asp Thr Ala Asn Ala Ser Thr Ser Asn Lys Gln Val
    595             600             605

Val Gly Val Pro Lys Val Gln Ala Asn Leu Leu Ala Glu Tyr Ser Leu
    610             615             620

Pro Ser Ile Pro Glu Trp Val Tyr Ser Ala Asn Val His Tyr Thr Gly
625             630             635             640

Lys Arg Ala Ala Asn Asp Thr Asn Thr Ser Tyr Ala Ser Ser Tyr Thr
            645             650             655

Thr Trp Asp Leu Gly Thr Arg Tyr Thr Thr Lys Val Ser Asn Val Pro
            660             665             670
```

Thr Thr Phe Arg Val Val Val Asn Asn Val Phe Asp Lys His Tyr Trp
        675   680   685

Ala Ser Ile Phe Pro Ser Gly Thr Asp Gly Asp Asn Gly Ser Pro Ser
        690   695   700

Ala Phe Ile Gly Gly Gly Arg Glu Val Arg Ala Ser Val Thr Phe Asp
705   710   715   720

Phe

<210>   50
<211>   669
<212>   PRT
<213>   Escherichia coli
<400>   50

Met Lys Asn Ile Thr Leu Trp Gln Arg Leu Arg Gln Val Ser Ile Ser
1   5   10   15

Thr Ser Leu Arg Cys Ala Phe Leu Met Gly Ala Leu Leu Thr Leu Ile
            20   25   30

Val Ser Ser Val Ser Leu Tyr Ser Trp His Glu Gln Ser Ser Gln Ile
        35   40   45

Arg Tyr Ser Leu Asp Lys Tyr Phe Pro Arg Ile His Ser Ala Phe Leu
    50   55   60

Ile Glu Gly Asn Leu Asn Leu Val Val Asp Gln Leu Asn Glu Phe Leu
65   70   75   80

Gln Ala Pro Asn Thr Thr Val Arg Leu Gln Leu Arg Thr Gln Ile Ile
                85   90   95

Gln His Leu Asp Thr Ile Glu Arg Leu Ser Arg Gly Leu Ser Ser Arg
            100   105   110

Glu Arg Gln Gln Leu Thr Val Ile Leu Gln Asp Ser Arg Ser Leu Leu
    115   120   125

Ser Glu Leu Asp Arg Ala Leu Tyr Asn Met Phe Leu Leu Arg Glu Lys

```
             130                    135                    140

Val Ser Glu Leu Ser Ala Arg Ile Asp Trp Leu His Asp Asp Phe Thr
145                 150                 155                 160

Thr Glu Leu Asn Ser Leu Val Gln Asp Phe Thr Trp Gln Gln Gly Thr
                165                 170                 175

Leu Leu Asp Gln Ile Ala Ser Arg Gln Gly Asp Thr Ala Gln Tyr Leu
                180                 185                 190

Lys Arg Ser Arg Glu Val Gln Asn Glu Gln Gln Gln Val Tyr Thr Leu
                195                 200                 205

Ala Arg Ile Glu Asn Gln Ile Val Asp Asp Leu Arg Asp Arg Leu Asn
        210                 215                 220

Glu Leu Lys Ser Gly Arg Asp Asp Asp Ile Gln Val Glu Thr His Leu
225                 230                 235                 240

Arg Tyr Phe Glu Asn Leu Lys Lys Thr Ala Asp Glu Asn Ile Arg Met
                245                 250                 255

Leu Asp Asp Trp Pro Gly Thr Ile Thr Leu Arg Gln Thr Ile Asp Glu
                260                 265                 270

Leu Leu Asp Met Gly Ile Val Lys Asn Lys Met Pro Asp Thr Met Arg
        275                 280                 285

Glu Tyr Val Ala Ala Gln Lys Ala Leu Glu Asp Ala Ser Arg Thr Arg
290                 295                 300

Glu Ala Thr Gln Gly Arg Phe Arg Thr Leu Leu Glu Ala Gln Leu Gly
305                 310                 315                 320

Ser Thr His Gln Gln Met Gln Met Phe Asn Gln Arg Met Glu Gln Ile
                325                 330                 335

Val His Val Ser Gly Gly Leu Ile Leu Val Ala Thr Ala Leu Ala Leu
                340                 345                 350

Leu Leu Ala Trp Val Phe Asn His Tyr Phe Ile Arg Ser Arg Leu Val
        355                 360                 365
```

```
Lys Arg Phe Thr Leu Leu Asn Gln Ala Val Val Gln Ile Gly Leu Gly
    370             375             380

Gly Thr Glu Thr Thr Ile Pro Val Tyr Gly Asn Asp Glu Leu Gly Arg
385             390             395                         400

Ile Ala Gly Leu Leu Arg His Thr Leu Gly Gln Leu Asn Val Gln Lys
                405             410             415

Gln Gln Leu Glu Gln Glu Ile Thr Asp Arg Lys Val Ile Glu Ala Asp
            420             425             430

Leu Arg Ala Thr Gln Asp Glu Leu Ile Gln Thr Ala Lys Leu Ala Val
        435             440             445

Val Gly Gln Thr Met Thr Thr Leu Ala His Glu Ile Asn Gln Pro Leu
    450             455             460

Asn Ala Leu Ser Met Tyr Leu Phe Thr Ala Arg Arg Ala Ile Glu Gln
465             470             475                         480

Thr Gln Lys Glu Gln Ala Ser Met Met Leu Gly Lys Ala Glu Gly Val
            485             490             495

Ile Ser Arg Ile Asp Ala Ile Ile Arg Ser Leu Arg Gln Phe Thr Arg
            500             505             510

Arg Ala Glu Leu Glu Thr Ser Leu His Ala Val Asp Leu Ala Gln Met
        515             520             525

Phe Ser Ala Ala Trp Glu Leu Leu Ala Met Arg His Arg Ser Leu Gln
    530             535             540

Ala Thr Leu Val Leu Pro Gln Gly Thr Ala Thr Val Ser Gly Asp Glu
545             550             555                         560

Val Arg Thr Gln Gln Val Leu Val Asn Val Leu Ala Asn Ala Leu Asp
            565             570             575

Val Cys Gly Gln Gly Ala Val Ile Thr Val Asn Trp Gln Met Gln Gly
            580             585             590
```

```
Lys Thr Leu Asn Val Phe Ile Gly Asp Asn Gly Pro Gly Trp Pro Glu
        595             600             605

Ala Leu Leu Pro Ser Leu Leu Lys Pro Phe Thr Thr Ser Lys Glu Val
    610             615                 620

Gly Leu Gly Ile Gly Leu Ser Ile Cys Val Ser Leu Met Glu Gln Met
625             630             635                 640

Lys Gly Glu Leu Arg Leu Ala Ser Thr Met Thr Arg Asn Ala Cys Val
            645             650                 655

Val Leu Gln Phe Arg Leu Thr Asp Val Glu Asp Ala Lys
            660             665
```

```
<210>   51
<211>   753
<212>   PRT
<213>   Escherichia coli
<400>   51
```

```
Met Asn Val Ile Lys Leu Ala Ile Gly Ser Gly Ile Leu Leu Leu Ser
1               5               10              15

Cys Gly Ala Tyr Ser Gln Ser Ile Ser Glu Lys Thr Asn Ser Asp Lys
            20              25              30

Lys Gly Ala Ala Glu Phe Ser Pro Leu Ser Val Ser Val Gly Lys Thr
        35              40              45

Thr Ser Glu Gln Glu Ala Leu Glu Lys Thr Gly Ala Thr Ser Ser Arg
    50              55              60

Thr Thr Asp Lys Asn Leu Gln Ser Leu Asp Ala Thr Val Arg Ser Met
65              70              75              80

Pro Gly Thr Tyr Thr Gln Ile Asp Pro Gly Gln Gly Ala Ile Ser Val
            85              90              95

Asn Ile Arg Gly Met Ser Gly Phe Gly Arg Val Asn Thr Met Val Asp
            100             105             110

Gly Ile Thr Gln Ser Phe Tyr Gly Thr Ser Thr Ser Gly Thr Thr Thr
        115             120             125
```

His Gly Ser Thr Asn Asn Met Ala Gly Val Leu Ile Asp Pro Asn Leu
    130   135   140

Leu Val Ala Val Asp Val Thr Arg Gly Asp Ser Ser Gly Ser Glu Gly
145   150   155   160

Ile Asn Ala Leu Ala Gly Ser Ala Asn Met Arg Thr Ile Gly Val Asp
            165   170   175

Asp Val Ile Phe Asn Gly Asn Thr Tyr Gly Leu Arg Ser Arg Phe Ser
            180   185   190

Val Gly Ser Asn Gly Leu Gly Arg Ser Gly Met Ile Ala Leu Gly Gly
        195   200   205

Lys Ser Asp Ala Phe Thr Asp Thr Gly Ser Ile Gly Val Met Ala Ala
    210   215   220

Val Ser Gly Ser Ser Val Tyr Ser Asn Phe Ser Asn Gly Ser Gly Ile
225   230   235   240

Asn Ser Lys Glu Phe Gly Tyr Asp Lys Tyr Met Lys Gln Asn Pro Lys
            245   250   255

Ser Gln Leu Tyr Lys Met Asp Ile Arg Pro Asp Glu Phe Asn Ser Phe
            260   265   270

Glu Leu Ser Ala Arg Thr Tyr Glu Asn Lys Phe Thr Arg Arg Asp Ile
        275   280   285

Thr Ser Asp Asp Tyr Tyr Ile Lys Tyr His Tyr Thr Pro Phe Ser Glu
    290   295   300

Leu Ile Asp Phe Asn Val Thr Ala Ser Thr Ser Arg Gly Asn Gln Lys
305   310   315   320

Tyr Arg Asp Gly Ser Leu Tyr Thr Phe Tyr Lys Thr Ser Ala Gln Asn
            325   330   335

Arg Ser Asp Ala Leu Asp Ile Asn Asn Thr Ser Arg Phe Thr Val Ala
            340   345   350

```
Asp Asn Asp Leu Glu Phe Met Leu Gly Ser Lys Leu Met Arg Thr Arg
        355             360             365

Tyr Asp Arg Thr Ile His Ser Ala Ala Gly Asp Pro Lys Ala Asn Gln
    370             375             380

Glu Ser Ile Glu Asn Asn Pro Phe Ala Pro Ser Gly Gln Gln Asp Ile
385             390             395             400

Ser Ala Leu Tyr Thr Gly Leu Lys Val Thr Arg Gly Ile Trp Glu Ala
            405             410             415

Asp Phe Asn Leu Asn Tyr Thr Arg Asn Arg Ile Thr Gly Tyr Lys Pro
            420             425             430

Ala Cys Asp Ser Arg Val Ile Cys Val Pro Gln Gly Ser Tyr Asp Ile
        435             440             445

Asp Asp Lys Glu Gly Gly Phe Asn Pro Ser Val Gln Leu Ser Ala Gln
    450             455             460

Val Thr Pro Trp Leu Gln Pro Phe Ile Gly Tyr Ser Lys Ser Met Arg
465             470             475             480

Ala Pro Asn Ile Gln Glu Met Phe Phe Ser Asn Ser Gly Gly Ala Ser
            485             490             495

Met Asn Pro Phe Leu Lys Pro Glu Arg Ala Glu Thr Trp Gln Ala Gly
        500             505             510

Phe Asn Ile Asp Thr Arg Asp Leu Leu Val Glu Gln Asp Ala Leu Arg
        515             520             525

Phe Lys Ala Leu Ala Tyr Arg Ser Arg Ile Gln Asn Tyr Ile Tyr Ser
    530             535             540

Glu Ser Tyr Leu Val Cys Ser Gly Gly Arg Lys Cys Ser Leu Pro Glu
545             550             555             560

Val Ile Gly Asn Gly Trp Glu Gly Ile Ser Asp Glu Tyr Ser Asp Asn
            565             570             575
```

```
Met Tyr Ile Tyr Val Asn Ser Ala Ser Asp Val Ile Ala Lys Gly Phe
        580             585             590

Glu Leu Glu Met Asp Tyr Asp Ala Gly Phe Ala Phe Gly Arg Leu Ser
        595             600             605

Phe Ser Gln Gln Gln Thr Asp Gln Pro Thr Ser Ile Ala Ser Thr His
    610             615             620

Phe Gly Ala Gly Asp Ile Thr Glu Leu Pro Arg Lys Tyr Met Thr Leu
625             630             635             640

Asp Thr Gly Val Arg Phe Phe Asp Asn Ala Leu Thr Leu Gly Thr Ile
            645             650             655

Ile Lys Tyr Thr Gly Lys Ala Arg Arg Leu Ser Pro Asp Phe Glu Gln
        660             665             670

Asp Glu His Thr Gly Ala Ile Ile Lys Gln Asp Leu Pro Gln Ile Pro
        675             680             685

Thr Ile Ile Asp Leu Tyr Gly Thr Tyr Glu Tyr Asn Arg Asn Leu Thr
        690             695             700

Leu Lys Leu Ser Val Gln Asn Leu Met Asn Arg Asp Tyr Ser Glu Ala
705             710             715             720

Leu Asn Lys Leu Asn Met Met Pro Gly Leu Gly Asp Glu Thr His Pro
            725             730             735

Ala Asn Ser Ala Arg Gly Arg Thr Trp Ile Phe Gly Gly Asp Ile Arg
            740             745             750

Phe
```

```
<210>  52
<211>  133
<212>  PRT
<213>  Escherichia coli
<400>  52
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```
Met Ser Ser Lys Thr Lys Cys Trp Leu Trp Met Leu Leu Val Ile Leu
1               5               10              15
```

```
Ser Glu Thr Ser Ala Thr Ser Thr Leu Lys Met Phe Asp Asn Ser Glu
        20              25                  30

Gly Met Thr Lys Thr Leu Leu Leu Ala Leu Ile Val Val Leu Tyr Cys
        35              40                  45

Ile Cys Tyr Tyr Ser Leu Ser Arg Ala Val Lys Asp Ile Pro Val Gly
    50              55                  60

Leu Ala Tyr Ala Thr Trp Ser Gly Thr Gly Ile Leu Met Val Ser Thr
65              70                  75                  80

Leu Gly Ile Leu Phe Tyr Gly Gln His Pro Asp Thr Ala Ala Ile Ile
            85                  90                  95

Gly Met Val Ile Ile Ala Ser Gly Ile Ile Ile Met Asn Leu Phe Ser
            100             105                 110

Lys Met Gly Ser Glu Glu Ala Glu Glu Thr Pro Val Thr Asn Leu Asp
        115             120                 125

Lys Lys Ile Ala Asn
        130


<210>   53
<211>   286
<212>   PRT
<213>   Escherichia coli
<400>   53

Met Tyr Ile Lys Lys His Trp Ile Ala Leu Ser Ile Leu Leu Ile Pro
1               5                   10                  15

Cys Ile Gly Asn Ala Gln Glu Ile Lys Ile Asp Glu Ser Trp Leu His
            20                  25                  30

Gln Ser Leu Asn Val Ile Gly Arg Thr Asp Ser Arg Phe Gly Pro Arg
        35                  40                  45

Leu Thr Asn Asp Leu Tyr Pro Glu Tyr Thr Val Ala Gly Arg Lys Asp
    50                  55                  60

Trp Phe Asp Phe Tyr Gly Tyr Val Asp Leu Pro Lys Phe Phe Gly Val
65                  70                  75                  80
```

```
Gly Ser His Tyr Asp Val Gly Ile Trp Asp Glu Gly Ser Pro Leu Phe
            85              90              95

Thr Glu Ile Glu Pro Arg Phe Ser Ile Asp Lys Leu Thr Gly Leu Asn
            100             105             110

Leu Ala Phe Gly Pro Phe Lys Glu Trp Phe Ile Ala Asn Asn Tyr Val
            115             120             125

Tyr Asp Met Gly Asp Asn Gln Ser Ser Arg Gln Ser Thr Trp Tyr Met
    130             135             140

Gly Leu Gly Thr Asp Ile Asp Thr Gly Leu Pro Ile Lys Leu Ser Ala
145             150             155             160

Asn Ile Tyr Ala Lys Tyr Gln Trp Gln Asn Tyr Gly Ala Ala Asn Glu
            165             170             175

Asn Glu Trp Asp Gly Tyr Arg Phe Lys Ile Lys Tyr Ser Ile Pro Leu
            180             185             190

Thr Asn Leu Phe Gly Gly Arg Leu Val Tyr Asn Ser Phe Thr Asn Phe
            195             200             205

Asp Phe Gly Ser Asp Leu Ala Asp Lys Ser His Asn Asn Lys Arg Thr
    210             215             220

Ser Asn Ala Ile Ala Ser Ser His Ile Leu Ser Leu Leu Tyr Glu His
225             230             235             240

Trp Lys Phe Ala Phe Thr Leu Arg Tyr Phe His Asn Gly Gly Gln Trp
            245             250             255

Asn Ala Gly Glu Lys Val Asn Phe Gly Asp Gly Pro Phe Glu Leu Lys
            260             265             270

Asn Thr Gly Trp Gly Thr Tyr Thr Thr Ile Gly Tyr Gln Phe
            275             280             285
```

<210> 54
<211> 172
<212> PRT

<213>   Escherichia coli
<400>   54

Met Arg Ile Ala Pro Arg Thr Phe Phe Ala Ile Ser Ala Leu Ala Phe
1   5   10   15

Ile Val Ala Ser Gly Phe Ser Phe Trp Arg Leu Ser Pro Ala Glu Asn
            20   25   30

Thr Gly Ile Met Ser Cys Ser Thr Lys Gly Ile Met Arg Phe Glu Asn
            35   40   45

Met Glu Lys Glu Asn Val Asn Gly Asn Ile His Phe Asn Phe Gly Ser
        50   55   60

Gln Gly Lys Gly Ser Met Val Leu Glu Gly Tyr Thr Asp Ser Ala Ala
65   70   75   80

Gly Trp Leu Tyr Leu Gln Arg Tyr Val Lys Phe Thr Tyr Thr Ser Lys
            85   90   95

Arg Val Ser Ala Thr Glu Arg His Tyr Arg Ile Ser Gln Trp Glu Ser
            100   105   110

Ser Ala Ser Ser Ile Asp Glu Ser Pro Asp Val Ile Phe Asp Tyr Phe
        115   120   125

Met Arg Glu Met Ser Asp Ser His Asp Gly Leu Phe Leu Asn Ala Gln
    130   135   140

Lys Leu Asn Asp Lys Ala Ile Leu Leu Ser Ser Ile Asn Ser Pro Leu
145   150   155   160

Trp Ile Cys Thr Leu Lys Ser Gly Ser Lys Leu Asp
            165   170

<210>   55
<211>   182
<212>   PRT
<213>   Escherichia coli
<400>   55

Met Lys Ile Lys Val Ile Ala Leu Ala Thr Phe Val Ser Ala Val Phe
1   5   10   15

Ala Gly Ser Ala Met Ala Tyr Asp Gly Thr Ile Thr Phe Thr Gly Lys
            20   25   30

Val Val Ala Gln Thr Cys Thr Val Asn Thr Ser Asp Lys Asp Leu Ala
            35   40   45

Val Thr Leu Pro Thr Val Ala Thr Ser Ser Leu Lys Asp Asn Ala Ala
            50   55   60

Thr Ser Gly Leu Thr Pro Phe Ala Ile Arg Leu Thr Gly Cys Ala Thr
65   70   75   80

Gly Met Asn Ser Ala Gln Asn Val Lys Ala Tyr Phe Glu Pro Ser Ser
                85   90   95

Asn Ile Asp Leu Ala Thr His Asn Leu Lys Asn Thr Ala Thr Pro Thr
            100   105   110

Lys Ala Asp Asn Val Gln Ile Gln Leu Leu Asn Ser Asn Gly Thr Ser
            115   120   125

Thr Ile Leu Leu Gly Glu Ala Asp Asn Gly Gln Asp Val Gln Ser Glu
            130   135   140

Thr Ile Gly Ser Asp Gly Ser Ala Thr Leu Arg Tyr Met Ala Gln Tyr
145   150   155   160

Tyr Ala Thr Gly Gln Ser Thr Ala Gly Asp Val Lys Ala Thr Val His
                165   170   175

Tyr Thr Ile Ala Tyr Glu
            180

<210>   56
<211>   359
<212>   PRT
<213>   Escherichia coli
<400>   56

Met Lys Arg Ile Phe Phe Ile Pro Leu Phe Leu Ile Leu Leu Pro Lys
1   5   10   15

Leu Ala Val Ala Gly Pro Asp Asp Tyr Val Pro Ser Gln Ile Ala Val
            20   25   30

```
Asn Thr Ser Thr Leu Pro Gly Val Val Ile Gly Pro Ala Asp Ala His
        35                40                45

Thr Tyr Pro Arg Val Ile Gly Glu Leu Ala Gly Thr Ser Asn Gln Tyr
    50                55                60

Val Phe Asn Gly Gly Ala Ile Ala Leu Met Arg Gly Lys Phe Thr Pro
65                70                75                80

Ala Leu Pro Lys Ile Gly Ser Ile Thr Val Tyr Phe Pro Ser Arg Lys
            85                90                95

Gln Arg Asp Ser Ser Asp Phe Asp Ile Tyr Asp Ile Gly Val Ser Gly
            100               105               110

Leu Gly Ile Ile Ile Gly Met Ala Gly Tyr Trp Pro Ala Thr Pro Leu
        115               120               125

Val Pro Ile Asn Ser Ser Gly Ile Tyr Ile Asp Pro Val Gly Ala Asn
    130               135               140

Thr Asn Pro Asn Thr Tyr Asn Gly Ala Thr Ala Ser Phe Gly Ala Arg
145               150               155               160

Leu Phe Val Ala Phe Val Ala Thr Gly Arg Leu Pro Asn Gly Tyr Ile
            165               170               175

Thr Ile Pro Thr Arg Gln Leu Gly Thr Ile Leu Leu Glu Ala Lys Arg
        180               185               190

Thr Ser Leu Asn Asn Lys Gly Leu Thr Ala Pro Val Met Leu Asn Gly
    195               200               205

Gly Arg Ile Gln Val Gln Ser Gln Thr Cys Thr Met Gly Gln Lys Asn
    210               215               220

Tyr Val Val Pro Leu Asn Thr Val Tyr Gln Ser Gln Phe Thr Ser Leu
225               230               235               240

Tyr Lys Glu Ile Gln Gly Gly Lys Ile Asp Ile His Leu Gln Cys Pro
            245               250               255
```

Asp Gly Ile Asp Val Tyr Ala Thr Leu Thr Asp Ala Ser Gln Pro Val
            260   265   270

Asn Arg Thr Asp Ile Leu Thr Leu Ser Ser Glu Ser Thr Ala Lys Gly
            275   280   285

Phe Gly Ile Arg Leu Tyr Lys Asp Ser Asp Val Thr Ala Ile Ser Tyr
            290   295   300

Gly Glu Asp Ser Pro Val Lys Gly Asn Gly Ser Gln Trp His Phe Ser
305   310   315   320

Asp Tyr Arg Gly Glu Val Asn Pro His Ile Asn Leu Arg Ala Asn Tyr
                325   330   335

Ile Lys Ile Ala Asp Ala Thr Thr Pro Gly Ser Val Lys Ala Ile Ala
            340   345   350

Thr Ile Thr Phe Ser Tyr Gln
            355

<210>   57
<211>   844
<212>   PRT
<213>   Escherichia coli
<400>   57

Met Asn Ala Asn Asn Leu Ser Cys Leu Ile Tyr Cys Arg Cys Ser Leu
1   5   10   15

Leu Leu Phe Ala Ala Leu Gly Leu Thr Val Thr Asn His Ser Phe Ala
            20   25   30

Ala Glu Glu Ala Glu Phe Asp Ser Glu Phe Leu His Leu Asp Lys Gly
            35   40   45

Ile Asn Ala Ile Asp Ile Arg Arg Phe Ser His Gly Asn Pro Val Pro
        50   55   60

Glu Gly Arg Tyr Tyr Ser Asp Ile Tyr Val Asn Asn Val Trp Lys Gly
65   70   75   80

Lys Ala Asp Leu Gln Tyr Leu Arg Thr Ala Asn Thr Gly Ala Pro Thr
                85   90   95

```
Leu Cys Leu Thr Pro Glu Leu Leu Ser Leu Ile Asp Leu Val Lys Asp
            100             105             110


Thr Met Ser Gly Asn Thr Ser Cys Phe Pro Ala Ser Thr Gly Leu Ser
            115             120             125


Ser Ala Arg Ile Asn Phe Asp Leu Ser Thr Leu Arg Leu Asn Ile Glu
    130             135             140


Ile Pro Gln Ala Leu Leu Asn Thr Arg Pro Arg Gly Tyr Ile Ser Pro
145             150             155             160


Ala Gln Trp Gln Ser Gly Val Pro Ala Ala Phe Ile Asn Tyr Asp Ala
                165             170             175


Asn Tyr Tyr Gln Tyr Ser Ser Ser Gly Thr Ser Asn Glu Gln Thr Tyr
            180             185             190


Leu Gly Leu Lys Ala Gly Phe Asn Leu Trp Gly Trp Ala Leu Arg His
        195             200             205


Arg Gly Ser Glu Ser Trp Asn Asn Ser Tyr Pro Ala Gly Tyr Gln Asn
    210             215             220


Ile Glu Thr Ser Ile Met His Asp Leu Ala Pro Leu Arg Ala Gln Phe
225             230             235             240


Thr Leu Gly Asp Phe Tyr Thr Asn Gly Glu Leu Met Asp Ser Leu Ser
                245             250             255


Leu Arg Gly Val Arg Leu Ala Ser Asp Glu Arg Met Leu Pro Gly Ser
            260             265             270


Leu Arg Gly Tyr Ala Pro Ala Val Arg Gly Ile Ala Asn Ser Asn Ala
        275             280             285


Lys Val Thr Ile Tyr Gln Asn Ala His Ile Leu Tyr Glu Thr Thr Val
    290             295             300


Pro Ala Gly Pro Phe Val Ile Asn Asp Leu Tyr Pro Ser Gly Tyr Ala
305             310             315             320
```

```
Gly Asp Leu Leu Val Lys Ile Thr Glu Ser Asn Gly Gln Thr Arg Met
              325             330             335

Phe Thr Val Pro Phe Ala Ala Val Ala Gln Leu Ile Arg Pro Gly Phe
              340             345             350

Ser Arg Trp Gln Met Ser Val Gly Lys Tyr Arg Tyr Ala Asn Lys Thr
              355             360             365

Tyr Asn Asp Leu Ile Ala Gln Gly Thr Tyr Gln Tyr Gly Leu Thr Asn
    370             375             380

Asp Ile Thr Leu Asn Ser Gly Leu Thr Thr Ala Ser Gly Tyr Thr Ala
385             390             395             400

Gly Leu Ala Gly Leu Ala Phe Asn Thr Pro Leu Gly Ala Ile Ala Ser
              405             410             415

Asp Ile Thr Leu Ser Arg Thr Ala Phe Arg Tyr Ser Gly Val Thr Arg
              420             425             430

Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser
              435             440             445

Asn Thr Asn Ile Thr Leu Ala Ala Tyr Arg Tyr Ser Ser Lys Asp Phe
    450             455             460

Tyr His Leu Lys Asp Ala Leu Ser Ala Asn His Asn Ala Phe Ile Asp
465             470             475             480

Asp Val Ser Val Lys Ser Thr Ala Phe Tyr Arg Pro Arg Asn Gln Phe
              485             490             495

Gln Ile Ser Ile Asn Gln Glu Leu Gly Glu Lys Trp Gly Gly Met Tyr
              500             505             510

Leu Thr Gly Thr Thr Tyr Asn Tyr Trp Gly His Lys Gly Ser Arg Asn
              515             520             525

Glu Tyr Gln Ile Gly Tyr Ser Asn Phe Trp Lys Gln Leu Gly Tyr Gln
    530             535             540

Ile Gly Leu Ser Gln Ser Arg Asp Asn Glu Gln Gln Arg Arg Asp Asp
```

139

```
545                    550                    555                    560


Arg Phe Tyr Ile Asn Phe Thr Leu Pro Leu Gly Gly Ser Val Gln Ser
                565                    570                    575


Pro Val Phe Ser Thr Val Leu Asn Tyr Ser Lys Glu Glu Lys Asn Ser
                580                    585                    590


Ile Gln Thr Ser Ile Ser Gly Thr Gly Gly Glu Asp Asn Gln Phe Ser
                595                    600                    605


Tyr Gly Ile Ser Gly Asn Ser Gln Glu Asn Gly Pro Ser Gly Tyr Ala
    610                    615                    620


Met Asn Gly Gly Tyr Arg Ser Pro Tyr Val Asn Ile Thr Thr Thr Val
625                    630                    635                    640


Gly His Asp Thr Gln Asn Asn Asn Gln Arg Ser Phe Gly Ala Ser Gly
                645                    650                    655


Ala Val Val Ala His Pro Tyr Gly Val Thr Leu Ser Asn Asp Leu Ser
                660                    665                    670


Asp Thr Phe Ala Ile Ile His Ala Glu Gly Ala Gln Gly Ala Val Ile
    675                    680                    685


Asn Asn Ala Ser Gly Ser Arg Leu Asp Phe Trp Gly Asn Gly Val Val
    690                    695                    700


Pro Tyr Val Thr Pro Tyr Glu Lys Asn Gln Ile Ser Ile Asp Pro Ser
705                    710                    715                    720


Asn Leu Asp Leu Asn Val Glu Leu Ser Ala Thr Glu Gln Glu Ile Ile
                725                    730                    735


Pro Arg Ala Asn Ser Ala Thr Leu Val Lys Phe Asp Thr Lys Thr Gly
                740                    745                    750


Arg Ser Leu Leu Phe Asp Ile Arg Met Ser Thr Gly Asn Pro Pro Pro
    755                    760                    765


Met Ala Ser Glu Val Leu Asp Glu His Gly Gln Leu Ala Gly Tyr Val
770                    775                    780
```

```
Ala Gln Ala Gly Lys Val Phe Thr Arg Gly Leu Pro Glu Lys Gly His
785             790             795             800


Leu Ser Val Val Trp Gly Pro Asp Asn Lys Asp Arg Cys Ser Phe Val
            805             810             815


Tyr His Val Ala His Asn Lys Asp Asp Met Gln Ser Gln Leu Val Pro
            820             825             830


Val Leu Cys Ile Gln His Pro Asn Gln Glu Lys Thr
        835             840
```

```
<210>  58
<211>  277
<212>  PRT
<213>  Escherichia coli
<400>  58
```

```
Met Val Lys Cys His Thr Leu Ile Asn Arg Arg Asn Lys Cys Leu Leu
1           5               10              15


Ile Val Phe Ile Val Leu Ile Gly Trp Ile Ile Phe Arg Pro Lys Ala
            20              25              30


Tyr Thr Tyr Ser Leu Asn Asp Lys Glu Lys Glu Met Leu Ile Met Leu
        35              40              45


Ser Gln His Pro Glu Thr Arg Tyr Phe Gly Phe Tyr Ser Ile Glu Leu
    50              55              60


Pro Ala Asp Tyr Lys Pro Thr Gly Met Val Met Phe Ile Gln Gly Ser
65              70              75              80


Ala Met Ile Pro Val Glu Thr Lys Leu Gln Tyr Tyr Pro Pro Phe Leu
            85              90              95


Gln Tyr Met Thr Arg Tyr Glu Ala Glu Leu Lys Asn Thr Ser Ala Leu
            100             105             110


Asp Pro Leu Asp Thr Pro Tyr Leu Lys Gln Val His Pro Leu Ser Pro
        115             120             125


Pro Met Asn Gly Val Ile Phe Glu Arg Met Lys Ala Lys Tyr Thr Pro
```

```
        130                    135                    140


Asp Phe Ala Arg Val Leu Asp Ala Trp Lys Trp Glu Asn Gly Val Thr
145             150             155                 160


Phe Ser Val Lys Ile Glu Ala Lys Asp Gly Arg Ala Thr Arg Tyr Asp
                165             170             175


Gly Ile Ser Lys Ile Ala Glu Tyr Ser Tyr Gly Tyr Asn Ile Pro Glu
            180             185             190


Lys Lys Val Gln Leu Leu Thr Ile Leu Ser Gly Leu Gln Pro Arg Ala
        195             200             205


Asp Asn Gln Pro Pro Ser Glu Asn Lys Leu Ala Ile Gln Tyr Ala Gln
    210             215             220


Val Asp Ala Ser Leu Leu Gly Glu Tyr Glu Leu Ser Val Asp Tyr Lys
225             230             235                 240


Asn Ser Asn Asn Ile Lys Ile Ser Leu Gln Thr Asp Asn Asn Ser Tyr
            245             250             255


Ile Asp Ser Leu Leu Asp Ile Arg Tyr Pro Ser Asn Gly Asn Arg Ala
            260             265             270


Trp Tyr Asn Ser Ile
        275


<210>   59
<211>   366
<212>   PRT
<213>   Escherichia coli
<400>   59

Met Leu Pro Glu Pro Val Tyr Arg Arg Trp Ile Ile Leu Leu Ile Ser
1               5               10                  15


Met Leu Thr Val Gly Thr Leu Phe Ile Leu Ser Val Trp Asn Ser Ala
            20              25              30


Thr Tyr Trp Asp Ile Phe Ile Tyr Gly Val Leu Pro Met Leu Phe Leu
        35              40              45
```

Trp Leu Cys Leu Phe Gly Ile Ala Leu Asn Lys Tyr Glu Gln Ser Val
    50   55   60

Ala Ala Cys Ile Ser Trp Glu Ser Glu Arg Gln Gln Val Lys Gln Leu
65   70   75   80

Trp Gln His Trp Ser Gln Lys Gln Leu Ala Ile Val Gly Asn Val Leu
            85   90   95

Phe Thr Pro Glu Glu Lys Gly Met Ser Val Leu Leu Gly Pro Gln Glu
            100   105   110

Glu Ile Pro Ala Tyr Pro Lys Lys Ala Arg Pro Leu Phe Ser Ala Ser
        115   120   125

Arg Tyr Ser Leu Ser Ser Ile Phe His Asp Ile His Gln Gln Leu Thr
    130   135   140

Gln Gln Phe Pro Asp Tyr Arg His Tyr Leu His Thr Ile Tyr Val Leu
145   150   155   160

Gln Pro Glu Lys Trp Arg Gly Glu Thr Val Arg Gln Ala Ile Phe His
                165   170   175

Gln Trp Asp Leu Val Pro Glu Arg Thr Asn Thr Leu Asn Gln Ile Gln
            180   185   190

Ser Leu Tyr Asp Glu Arg Phe Asp Gly Leu Ile Leu Val Val Cys Leu
    195   200   205

Gln Asn Trp Pro Glu Asn Lys Pro Glu Asp Thr Ser Glu Leu Val Ser
    210   215   220

Ala Gln Leu Ile Ser Ser Ser Ser Phe Val Arg Gln His Gln Ile Pro
225   230   235   240

Val Ile Ala Gly Leu Gly Arg Val Met Pro Leu Glu Pro Glu Glu Leu
            245   250   255

Glu His Asn Leu Asp Val Leu Phe Glu Tyr Asn Gln Leu Asp Asn Lys
            260   265   270

Gln Leu Gln His Val Trp Val Ser Gly Leu Asp Glu Gly Thr Ile Glu

```
            275                    280                    285

Asn Leu Met Gln Tyr Ala Glu Gln His Gln Trp Ser Leu Pro Lys Lys
        290                    295                    300

Arg Pro Leu His Met Ile Asp His Ser Phe Gly Pro Thr Gly Glu Phe
305                    310                    315                    320

Ile Phe Pro Val Ser Leu Ala Met Leu Ser Glu Ala Ala Lys Glu Thr
                325                    330                    335

Glu Gln Asn His Leu Ile Ile Tyr Gln Ser Ala Gln Tyr Ala Gln Lys
                340                    345                    350

Lys Ser Leu Cys Leu Ile Thr Arg Lys Leu Tyr Leu Arg Thr
                355                    360                    365


<210>   60
<211>   260
<212>   PRT
<213>   Escherichia coli
<400>   60

Met Leu Asn Arg Lys Leu Asn Ile Arg Leu Arg His Ser Leu Asn Ser
1               5                   10                   15

His Cys Ile Pro Ser Ile Ile Ile Asn Asn Thr Val Arg Ser Phe Gln
                20                  25                   30

Arg Ser Val Met Asn Thr Arg Ala Leu Phe Pro Leu Leu Phe Thr Val
            35                  40                   45

Ala Ser Phe Ser Ala Ser Ala Gly Asn Trp Ala Val Lys Asn Gly Trp
        50                  55                   60

Cys Gln Thr Met Thr Glu Asp Gly Gln Ala Leu Val Met Leu Lys Asn
65                  70                   75                   80

Gly Thr Ile Gly Ile Thr Gly Leu Met Gln Gly Cys Pro Asn Gly Val
                85                  90                   95

Gln Thr Leu Leu Gly Ser Arg Ile Ser Ile Asn Gly Asn Leu Ile Pro
            100                 105                  110
```

Thr Ser Gln Met Cys Asn Gln Gln Thr Gly Phe Arg Ala Val Glu Val
        115   120   125

Glu Ile Gly Gln Ala Pro Glu Met Val Lys Lys Ala Val His Ser Ile
        130   135   140

Ala Glu Arg Asp Val Ser Val Leu Gln Ala Phe Gly Val Arg Met Glu
145   150   155   160

Phe Thr Arg Gly Asp Met Leu Lys Val Cys Pro Lys Phe Val Thr Ser
                165   170   175

Leu Ala Gly Phe Ser Pro Lys Gln Thr Thr Thr Ile Asn Lys Asp Ser
                180   185   190

Val Leu Gln Ala Ala Arg Gln Ala Tyr Ala Arg Glu Tyr Asp Glu Glu
        195   200   205

Thr Thr Glu Thr Ala Asp Phe Gly Ser Tyr Glu Val Lys Gly Asn Lys
        210   215   220

Val Glu Phe Glu Val Phe Asn Pro Glu Asp Arg Ala Tyr Asp Lys Val
225   230   235   240

Thr Val Thr Val Gly Ala Asp Gly Asn Ala Thr Gly Ala Ser Val Glu
                245   250   255

Phe Ile Gly Lys
        260

<210> 61
<211> 385
<212> PRT
<213> Escherichia coli
<400> 61

Val Val Ile Ile Asn Ser Thr Ile Leu Ser Gly Ala Gly Ala Ile Pro
1   5   10   15

Ser Leu Thr Ser Leu Leu Pro Asp Ile Arg Lys Met Leu Leu Val Thr
        20   25   30

Asp Arg Asn Ile Ala Gln Leu Asp Gly Val Gln Gln Ile Arg Ala Leu
        35   40   45

```
Leu Glu Lys His Cys Pro Gln Val Asn Val Ile Asp Asn Val Pro Ala
    50              55              60

Glu Pro Thr His His Asp Val Arg Gln Leu Met Asp Ala Pro Gly Asp
65              70              75              80

Ala Ser Phe Asp Val Val Val Gly Ile Gly Gly Gly Ser Val Leu Asp
            85              90              95

Val Ala Lys Leu Leu Ser Val Leu Cys His Pro Gln Ser Pro Gly Leu
        100             105             110

Asp Ala Leu Leu Ala Gly Glu Lys Pro Thr Gln Arg Val Gln Ser Trp
        115             120             125

Leu Ile Pro Thr Thr Ala Gly Thr Gly Ser Glu Ala Thr Pro Asn Ala
    130             135             140

Ile Leu Ala Ile Pro Glu Gln Ser Thr Lys Val Gly Ile Ile Ser Gln
145             150             155             160

Val Leu Leu Pro Asp Tyr Val Ala Leu Phe Pro Glu Leu Thr Thr Ser
            165             170             175

Met Pro Ala His Ile Ala Ala Ser Thr Gly Ile Asp Ala Leu Cys His
        180             185             190

Leu Leu Glu Cys Phe Thr Ala Thr Val Ala Asn Pro Val Ser Asp Asn
        195             200             205

Ala Ala Leu Thr Gly Leu Ser Lys Leu Phe Arg His Ile Gln Pro Ala
210             215             220

Val Asn Asp Pro Gln Asp Leu Arg Ala Lys Leu Glu Met Leu Trp Ala
225             230             235             240

Ser Tyr Tyr Gly Gly Val Ala Ile Thr His Ala Gly Thr His Leu Val
            245             250             255

His Ala Leu Ser Tyr Pro Leu Gly Gly Lys Tyr His Leu Pro His Gly
        260             265             270
```

146

```
Val Ala Asn Ala Ile Leu Leu Ala Pro Cys Met Ala Phe Val Arg Pro
        275                 280                 285


Trp Ala Val Glu Lys Phe Ala Arg Val Trp Asp Cys Ile Pro Asp Ala
    290                 295                 300


Glu Thr Ala Leu Ser Ala Glu Glu Lys Ser His Ala Leu Val Thr Trp
305                 310                 315                 320


Leu Gln Ala Leu Val Asn Gln Leu Lys Leu Pro Asn Asn Leu Ala Ala
            325                 330                 335


Leu Gly Val Pro Pro Glu Asp Ile Ala Ser Leu Ser Glu Ala Ala Leu
            340                 345                 350


Asn Val Lys Arg Leu Met Asn Asn Val Pro Cys Gln Ile Asp Leu Gln
        355                 360                 365


Asp Val Gln Ala Ile Tyr Gln Thr Leu Phe Pro Gln His Pro Phe Lys
    370                 375                 380


Glu
385


<210>   62
<211>   105
<212>   PRT
<213>   Escherichia coli
<400>   62

Met Asn Ile Arg Lys Leu Phe Cys Pro Gly Asn Thr Pro Arg Ile Leu
1               5                   10                  15


Leu Phe Leu Phe Phe Phe Val Val Ser Ala Ile Thr Thr Ile Ala Cys
            20                  25                  30


Gly Tyr Thr Glu Lys Asn Ala Thr Gly Asn Val Leu Leu Leu Phe Leu
        35                  40                  45


Leu Leu Leu Leu Ala His Arg Asn Thr Leu Thr Ser Ile Thr Ala Leu
    50                  55                  60


Leu Phe Leu Phe Cys Cys Ala Leu Tyr Ala Pro Ala Gly Met Thr Tyr
65                  70                  75                  80
```

147

```
Gly Lys Ile Asn Asn Ser Phe Ile Val Ala Leu Leu Gln Thr Thr Thr
            85              90              95

Asp Glu Ala Ala Glu Phe Thr Gly Met
            100             105


<210>   63
<211>   147
<212>   PRT
<213>   Escherichia coli
<400>   63

Met Asn Ile Gln Ala Ile Lys Glu Met Val Asn Leu Ile Cys Ser Phe
1               5               10              15

Leu Phe Ile Phe Phe Leu Ser Ser Ala Phe Val Ser Phe Gly Cys Tyr
            20              25              30

Ala Ile Tyr Glu Leu Phe Leu Trp Asn Asp Ile Ile Val Tyr Ser Trp
            35              40              45

Gly Tyr Ile Leu Ile Val Phe Leu Pro Phe Thr Leu Tyr Val Met Ser
    50              55              60

Phe Glu Ile Leu Phe Phe Ala Ile Ser Gly Arg Arg Leu Ser Lys Val
65              70              75              80

Thr Met Val Arg Leu Trp Leu Ile Ile Lys Ile Ile Ile Ala Phe Ser
            85              90              95

Ile Cys Ala Val Leu Ile Phe Ser Ser Ile Tyr Lys Lys Glu Leu Leu
            100             105             110

Ser Arg Asn Tyr Ile Ala Cys Ser Gly Ile Pro Ser Gly Trp Met Pro
            115             120             125

Gly Leu Ala Thr Lys Tyr Val Lys Glu Lys Ser Leu Cys Glu Lys Asn
    130             135             140

Gly Asn Asn
145


<210>   64
<211>   178
```

```
<212>    PRT
<213>    Escherichia coli
<400>    64
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Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
1   5   10   15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
            20   25   30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
        35   40   45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
    50   55   60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
65   70   75   80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
                85   90   95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
            100   105   110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
            115   120   125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
        130   135   140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
145   150   155   160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
                165   170   175

Asp Lys

```
<210>    65
<211>    209
<212>    PRT
<213>    Escherichia coli
<400>    65
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Met Phe Leu Lys Arg Lys Trp Tyr Tyr Ala Val Thr Thr Ser Val Val
1               5                   10                  15


Ile Thr Leu Cys Gly Gly Gly Tyr Tyr Met Tyr Arg Gln Glu Tyr Gln
                20                  25                  30


Met Val Val Thr Val Pro Thr Ala Asp Ala Asn Asp Pro Asn Trp Pro
            35                  40                  45


Asn Lys Arg Ile Gln Phe Asp Thr Ser Glu Trp Leu Gln Gln Leu Gln
        50                  55                  60


Tyr Ile Lys Ile Asp Asp His Tyr Ile Leu Asn Thr Gln Tyr Thr Pro
65                  70                  75                  80


Ile Ala Asn Leu Asp Asp Phe Gly Ile Thr Leu Lys Leu Gln Asn Ala
                85                  90                  95


Leu Asn Gly Ser Asp Lys Arg Leu Pro Ala Leu Tyr Gly Leu Ala Glu
            100                 105                 110


Met Asp Ala Gln Lys Phe Lys Asp Leu Met Arg Gly Lys Ile Lys Cys
        115                 120                 125


Glu Tyr Leu Arg Thr Thr Phe Asp Ala Glu Thr Leu Lys Pro Val Asn
    130                 135                 140


Asp Tyr Phe Leu Ile Ser Phe Thr Tyr Lys Asp Lys Trp Tyr Glu Phe
145                 150                 155                 160


Glu Thr Glu Arg Lys Ile Ser Lys Thr Ser Asp Asp Gly Tyr Phe Leu
            165                 170                 175


Trp Ala Phe Asp Asn Thr Val His Glu Ala Gly Tyr Trp His Asn Thr
            180                 185                 190


Asp Pro Ala Ala Tyr Ser Tyr Arg Asp Tyr Gln Asn Gly Lys Ala Val
            195                 200                 205


Lys
```

<210> 66
<211> 424
<212> PRT
<213> Escherichia coli
<400> 66

Met Asp Ile Trp Arg Gly His Ser Phe Leu Met Thr Ile Ser Ala Arg
1   5   10   15

Phe Arg Gln Tyr Val Phe Ser Leu Met Ser Ile Leu Leu Gln Glu Arg
            20   25   30

Lys Met Asn Ile Phe Thr Leu Ser Lys Ala Pro Leu Tyr Leu Leu Ile
            35   40   45

Ser Leu Phe Leu Pro Thr Met Ala Met Ala Ile Asp Pro Pro Glu Arg
        50   55   60

Glu Leu Ser Arg Phe Ala Leu Lys Thr Asn Tyr Leu Gln Ser Pro Asp
65   70   75   80

Glu Gly Val Tyr Glu Leu Ala Phe Asp Asn Ala Ser Lys Lys Val Phe
                85   90   95

Ala Ala Val Thr Asp Arg Val Asn Arg Glu Ala Asn Lys Gly Tyr Leu
            100   105   110

Tyr Ser Phe Asn Ser Asp Ser Leu Lys Val Glu Asn Lys Tyr Thr Met
        115   120   125

Pro Tyr Arg Ala Phe Ser Leu Ala Ile Asn Gln Asp Lys His Gln Leu
        130   135   140

Tyr Ile Gly His Thr Gln Ser Ala Ser Leu Arg Ile Ser Met Phe Asp
145   150   155   160

Thr Pro Thr Gly Lys Leu Val Arg Thr Ser Asp Arg Leu Ser Phe Lys
                165   170   175

Ala Ala Asn Ala Ala Asp Ser Arg Phe Glu His Phe Arg His Met Val
            180   185   190

Tyr Ser Gln Asp Ser Asp Thr Leu Phe Val Ser Tyr Ser Asn Met Leu
        195   200   205

```
Lys Thr Ala Glu Gly Met Lys Pro Leu His Lys Leu Leu Met Leu Asp
    210             215             220

Gly Thr Thr Leu Ala Leu Lys Gly Glu Val Lys Asp Ala Tyr Lys Gly
225             230             235             240

Thr Ala Tyr Gly Leu Thr Met Asp Glu Lys Thr Gln Lys Ile Tyr Val
            245             250             255

Gly Gly Arg Asp Tyr Ile Asn Glu Ile Asp Ala Lys Asn Gln Thr Leu
            260             265             270

Leu Arg Thr Ile Pro Leu Lys Asp Pro Arg Pro Gln Ile Thr Ser Val
        275             280             285

Gln Asn Leu Ala Val Asp Ser Ala Ser Asp Arg Ala Phe Val Val Val
    290             295             300

Phe Asp His Asp Asp Arg Ser Gly Thr Lys Asp Gly Leu Tyr Ile Phe
305             310             315             320

Asp Leu Arg Asp Gly Lys Gln Leu Gly Tyr Val His Thr Gly Ala Gly
            325             330             335

Ala Asn Ala Val Lys Tyr Asn Pro Lys Tyr Asn Glu Leu Tyr Val Thr
            340             345             350

Asn Phe Thr Ser Gly Thr Ile Ser Val Val Asp Ala Thr Lys Tyr Ser
        355             360             365

Ile Thr Arg Glu Phe Asn Met Pro Val Tyr Pro Asn Gln Met Val Leu
    370             375             380

Ser Asp Asp Met Asp Thr Leu Tyr Ile Gly Ile Lys Glu Gly Phe Asn
385             390             395             400

Arg Asp Trp Asp Pro Asp Val Phe Val Glu Gly Ala Lys Glu Arg Ile
            405             410             415

Leu Ser Ile Asp Leu Lys Lys Ser
            420
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<210>    67
<211>    489
<212>    DNA
<213>    Escherichia coli
<400>    67
atgaaactga aagctattat attggccacc ggtcttatta actgtattgt attttcagca      60

caggcagtgg atacgacgat tactgtgacg ggtaatgttt tgcaaagaac atgtaatgta     120

ccagggaatg tggatgtttc tttgggtaat ctgtatgtat cagactttcc caatgcagga     180

agtggatctc catgggttaa ttttgatctg tctctcaccg gatgccagaa tatgaatact     240

gttcgggcaa catttagtgg tactgcggat gggcagacat actatgcgaa tacagggaat     300

gctggcggta tcaagattga aattcaggac agggatggaa gtaatgcatc atatcacaat     360

ggtatgttca agacgcttaa tgtacaaaat aataatgcaa cctttaatct taaagcccgt     420

gcagtgagta aaggccaggt tactcctgga aatatcagtt ctgttataac cgtcacctat     480

acctatgcg                                                            489


<210>    68
<211>    2019
<212>    DNA
<213>    Escherichia coli
<400>    68
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aatgcccaga cttcacagca agacgaaagc acgctggtgg ttaccgccag taaacaatct     120

tcccgctcgg catcagccaa caacgtctcg tctactgttg tcagcgcgcc ggaattaagc     180

gacgccggcg tcaccgccag cgacaaactc cccagagtct tgcccgggct caatattgaa     240

aatagcggca acatgctttt ttcgacgatc tcgctacgcg gcgtctcttc agcgcaggac     300

ttctataacc ccgccgtcac cctgtatgtc gatggcgtcc ctcagctttc caccaacacc     360

atccaggcgc ttaccgatgt gcaaagcgtg gagttgctgc gaggcccaca gggaacgtta     420

tatggcaaaa gcgctcaggg cgggatcatc aacatcgtca cccagcagcc ggacagcacg     480

ccgcgcggct atattgaagg cggcgtcagt agccgcgaca gttatcgaag taagttcaac     540

ctgagcggcc ccattcagga tggcctgctg tacggcagcg tcaccctgtt acgccaggtt     600

gatgacggcg acatgattaa ccccgcgacg ggaagcgatg acttaggcgg cacccgcgcc     660

agcataggga atgtgaaact gcgtctggcg ccggacgatc agccctggga atgggctttt     720

gccgcctcac gcgaatgtac ccgcgccacc caggacgcct atgtgggatg gaatgatatt     780

aagggccgta agctgtcgat cagcgatggt tcaccagacc cgtacatgcg cgctgcact      840
```

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gacagccaga ccctgagtgg gaaatacacc accgatgact gggttttcaa cctgatcagc    900

gcctggcagc agcagcatta ttcgcgcacc ttcccttccg gttcgttaat cgtcaatatg    960

tctcagcgct ggaatcagga tgtgcaggag ctgcgcgctg caaccctggg cgatgcgcgt   1020

accgttgata tggtgtttgg gctgtaccgg cagaacaccc gcgagaagtt aaattcagcc   1080

tacgacatgc cgacaatgcc ttatttaagc agtaccggct ataccaccgc tgaaacgctg   1140

gccgcataca gtgacctgac ctggcattta accgatcgtt ttgatatcgg cggcggcgtg   1200

cgcttctcgc atgataaatc cagtacacaa tatcacggca gcatgctcgg caacccgttt   1260

ggcgaccagg gtaagagcaa tgacgatcag gtgctcgggc agctatccgc aggctatatg   1320

ctgaccgatg actggagagt gtatacccgt gtagcccagg atataaaacc ttccgggtac   1380

aacatcgtgc ctactgcggg tcttgatgcc aaaccgttcg tcgccgagaa atccatcaac   1440

tatgaacttg gcacccgcta cgaaaccgct gacgtcacgc tgcaagccgc gacgttttat   1500

acccacacca aagacatgca gctttactct ggcccggtcg ggatgcagac attaagcaat   1560

gcgggtaaag ccgacgccac cggcgttgag cttgaagcga gtggcggtt tgcgccaggc   1620

tggtcatggg atatcaatgg caacgtgatc cgttccgaat tcaccaatga cagtgagttg   1680

tatcacggta accgggtgcc gttcgtacca cgttatggcg cgggaagcag cgtgaacggc   1740

gtgattgata cgcgctatgg cgcactgatg ccccgactgg cggttaatct ggtcgggccg   1800

cattatttcg atggcgacaa ccagttgcgg caaggcacct atgccaccct ggacagcagc   1860

ctgggctggc aggcgactga acggatgaac atttccgtct atgtcgataa cctgttcgac   1920

cgtcgttacc gtacctatgg ctacatgaac ggcagcagcg ccgtcgcgca ggtcaatatg   1980

ggtcgcaccg tcggtatcaa tacgcgaatt gatttcttc                          2019
```

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<210>    69
<211>    738
<212>    DNA
<213>    Escherichia coli
<400>    69
atgaataagg ttttttgttgt ttcagtggtg gccgcagcct gtgtatttgc agtaaatgca     60

ggagcaaagg aaggtaaaag cggttttttat ctgaccggta agccggtgc ctctgtgatg    120

tcactttcag accagcgttt cctgtcagga gatgaggaag aaacatcaaa gtataaaggc    180

ggcgatgacc atgatacggt attcagtggc ggtattgcgg tcggttatga ttttttatccg   240

cagttcagta ttccggttcg tacagaactg gagtttttacg ctcgtggaaa agctgattcg   300

aagtataacg tagataaaga cagctggtca ggtggttact ggcgtgatga cctgaagaat   360
```

154

```
gaggtgtcag tcaacacact aatgctgaat gcgtactatg acttccggaa tgacagcgca      420

ttcacaccat gggtatccgc agggattggc tacgccagaa ttcaccagaa aacaaccggt      480

atcagtacct gggattatga gtacggaagc agtggtcgcg aatcgttgtc acgttcaggc      540

tctgctgaca acttcgcatg gagccttggc gcgggtgtcc gctatgacgt aaccccggat      600

atcgctctgg acctcagcta tcgctatctt gatgcaggtg acagcagtgt gagttacaag      660

gacgagtggg gcgataaata taagtcagaa gttgatgtta aaagtcatga catcatgctt      720

ggtatgactt ataacttc                                                    738
```

```
<210>    70
<211>    498
<212>    DNA
<213>    Escherichia coli
<400>    70
atgaaactga aagctattat attggccacc ggtcttatta actgtattgc attttcagca       60

caggcagtgg atacgacgat tactgttaca gggagggtat tgccacgtac ctgtaccatt      120

ggtaatggag gaaacccaaa cgccaccgtt gttttggata cgcttacac ttctgacctg       180

atagcagcca acagcacctc tcagtggaaa aatttttcgt tgacattgac gaattgtcag      240

aatgtaaaca atgttacttc atttggtgga accgcagaaa atacaaatta ttacagaaat      300

acaggggatg ctactaatat catggttgag ctacaggaac aaggtaatgg taatacccccc      360

ttgaaagttg gttcaacaaa agttgttaca gtgagcaatg ggcaggcgac attcaatctt      420

aaagtccgtg ccgtaagcaa aggtaatgct ggtgcgggaa gtattaattc acaaattact      480

gtcacctata cctatgcg                                                    498
```

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<210>    71
<211>    3885
<212>    DNA
<213>    Escherichia coli
<400>    71
atgaataaaa tatactccct taaatatagt gctgccactg gcggactcat tgctgtttct       60

gaattagcga aaagagtttc tggtaaaaca aaccgaaaac ttgtagcaac aatgttgtct      120

ctggctgttg ccggtacagt aaatgcagca atattgata tatcaaatgt atgggcgaga       180

gactatcttg atcttgcaca aaataaaggt attttccagc ccggagcaac agacgtaaca      240

atcactttaa aaaacggaga taaattctct ttccataatc tctcaattcc ggattttct       300

ggtgcagcag cgagtggcgc agctaccgca ataggaggtt cttatagtgt tactgttgca      360
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cataacaaaa agaaccctca ggccgcagaa acccaggttt acgctcagtc ttcttacagg    420

gttgttgaca gaagaaattc caatgatttt gagattcaga ggttaaataa atttgttgtg    480

gaaacagtag gtgccacccc ggcagagacc aaccctacaa catattctga tgcattagaa    540

cgctacggta tagtcacttc tgacggttca aaaaaaatca taggttttcg tgctggctct    600

ggaggaacat catttattaa tggtgaatcc aaaatctcaa caaattcagc atatagccat    660

gatctgttaa gtgctagtct atttgaggtc acccaatggg actcatacgg catgatgatt    720

tataaaaatg ataaaacatt tcgtaatctt gaaatattcg gagacagcgg ctctggagca    780

tacttatatg ataacaaact agaaaaatgg gtattagtcg gaacaaccca tggtattgcc    840

agcgttaatg gtgaccaact gacatggata acaaaataca atgataaact ggttagtgag    900

ttaaaagata cctatagtca taaaataaat ctgaatggca ataatgtaac cattaaaaac    960

acagatataa cattcacca aaacaatgca gataccactg gtactcaaga aaaaataact   1020

aaagacaaag atattgtgtt cacaaatggg ggagatgtcc tgtttaagga taatttggat   1080

tttggtagcg gtggtattat ctttgacgaa ggccatgaat ataacataaa cggtcaggga   1140

tttacattta aaggagcagg aattgatatc ggaaaagaaa gcattgtaaa ctggaatgca   1200

ttgtattcca gtgatgatgt tttacacaaa ataggccccg gtactctgaa tgttcaaaaa   1260

aaacagggggg caaatataaa gataggtgaa ggaaatgtta ttcttaatga agaaggaaca   1320

tttaacaata tataccttgc aagcggaaat ggtaaggtaa tactaaataa agataattcc   1380

cttggcaatg atcaatatgc ggggatattt tttactaaac gtggtggtac gctagattta   1440

aatggacaca atcagacttt tactagaatt gccgccactg acgatggaac aacaataact   1500

aactcagata caacgaaaga agccgttctg gcaatcaata acgaagactc ctacatatat   1560

catgggaaca taaatggcaa tataaaacta acgcacaata ttaattctca ggataagaaa   1620

actaatgcaa aattaattct ggatggtagt gtcaacacaa aaaatgatgt tgaagtcagt   1680

aatgccagtc ttaccatgca aggccatgca acagagcatg caatattcag aagctcagcg   1740

aatcattgct ccctggtatt tctttgtgga acggactggg tcaccgtttt gaaagaaaca   1800

gagagttcat ataataaaaa attcaattct gattacaaaa gtaataatca gcagacctca   1860

tttgatcagc ctgactggaa aaccggggtg tttaaatttg atacattaca cctgaacaat   1920

gctgactttt caatatcacg caatgccaat gttgaaggaa atatatcagc aaataaatca   1980

gctatcacaa tcggcgataa aaatgtttac attgataatc ttgcagggaa aaatattact   2040

aataatggtt ttgacttcaa acaaactatc agtactaatc tatccatagg agaaactaaa   2100
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```
tttacaggtg gcatcactgc acataacagc caaatagcca taggtgatca agctgtagtt    2160

acacttaatg gtgcaacctt tctggataat actcctataa gtatagataa aggagcaaaa    2220

gttatagcac aaaattccat gttcacaaca aaaggtattg atatctccgg tgaactgact    2280

atgatgggaa tccctgaaca gaatagtaaa actgtaacgc cgggtctcca ctacgctgct    2340

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acctttctg aaagcggtga ggctttccag atgaatatgg tgtacgcctt tggttttgac   840
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<213>   Escherichia coli
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atcactcatg ccggagtggt tcgtattgaa gggttaatta ccgaaaaaac ctgcattatt      120

tctgatgagt caaaaaattt tacagttaat atgccagacg tacccagtag ttcggtaagg      180

agtgcagggg atgttactga aaaggtttat:ttttccataa cgttaacccg ctgtggtagt     240

gatgttggca acgcgtatat aaagtttacc ggcaatacag tttctgaaga tgccagttta      300

tataagctgg aagatggctc ggtagagggg cttgcactta cgatttttga taagaacaaa      360

ggcagtatta gtaatgatgt taaaagcatg gttttttcac ttacatcatc agttgataat     420

atattgcatt tttttgcggc ttacaaagca ttaaaaaata atgtccaacc aggggatgca     480

aatgcgtcag tatcgtttat tgtcacctat gat                                   513
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```
<210>   81
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<211>    603
<212>    DNA
<213>    Escherichia coli
<400>    81
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ttggtatggc cgacggttat tgccttagcc gtacttatat tcacgttaac ttttctggcg       120

gaaataatat tctcctttcc gctcctggtt gtgcgtattt ctcttcagga attacaactt       180

gagttattgg ttgtatatgc actttttttc agtgtaatgg gtggcatcgg ttggcaattc       240

tcccgcagaa cgcctcctga attaaaaaac aggctacatt gctggctggt cttttctccg       300

gtctatttct ggttaattct ctcgaatttc attctttata tttctccaga gaaatcagcg       360

ttgctggaaa atatccgaaa tttctttctg acatttgtct ggcttcccct gaattttttcc      420

cctttttggc cgcagccgtg gactgatttt gtcggcccga ttagtgccca gcttggtttt       480

gcgttgggat attattgcca gtggcgtagc aaaaatagaa gccataggaa gaagtggggc       540

gattgggtaa cgtgcttaag tttggcgatt ttagctctgg ggccgttatt caattattta       600

caa                                                                      603


<210>    82
<211>    702
<212>    DNA
<213>    Escherichia coli
<400>    82
atgaaattca atttatctaa tttatccgca gtattactgg catcaggtat gctgatgtct        60

actgcggtaa ccgcagcacc cggcgatgca acacaatttg gtggggcgga tactgactgg       120

agcaccgttg attatcccag gctcactgat atggatgaca cgttgattc aatggggggg        180

aaaatccgct ttactggccg tgtagtgaaa gctacctgta aggtcgcaac cgattcaaaa       240

cagattgaag ttgtcctgcc ggttgtgcct tccaaccttt tcactggtat cgacgtagaa       300

gcacagggggc gagcaacca gaccgatttc aatattaatc tgaccgaatg tagcaataca       360

gatgatcaga aaattgagtt ccgtttttacc ggtactgcag atagcgctaa taaaacgctc       420

gctaacgaag tagaaggatc aacggatgct gacaacagcg gcaatgcggg ggcgactggt       480

gtagggattc gaatttactc caaaggtacg acgaataatg gtctgattaa cctgaatacc       540

actgcggcag agggtagcgc ctccaccgcc gcttatacaa ttccaggaaa tgctacgacc       600

catgatttca gcgcggcctt tactgcaggt tatgctcaaa acggtagcac tgttgcacca       660

ggtgtagtta agtcaacagc aagttttgtt gtgctgtacg ag                          702
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```
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<211>    1008
<212>    DNA
<213>    Escherichia coli
<400>    83
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ccgggttcac cgagtaataa tactacgcct gcatcctttt cttataattt tggtactata     180

gtggtttctg atgtcaacaa aaatgcgcct ggcactgtat tgccatcaca aatctggaag     240

gttggaacct ataaggctta ttgtaattct cttgatgatt atgaaattta cttcagtgct     300

gtctctggaa tagatccgtc tggtgccagt ggtgatcatc aagggagtga tgtatttatt     360

ccactcaccc atgaaatatc tgtctctact catataaaac tttataatca aaatggcaca     420

atgacagata aaattgtgcc attcgaaaat tataatacca attatccggg ggacagaagc     480

aaaccatcta attgggcatc aggtactgaa ggatatatta aaatcaggat tgataaaaaa     540

attatatctg atgtttcatt aagtaacgta ttattggtgt cattatatgt cagccagatc     600

cctaccgaac atggtcctat ccctgtcttt aatgcctaca taggaaactt aaatattcag     660

gttccgcaag gttgcactat taatgagggt acgagtttta ctgttaatat gccggatgtg     720

tgggccagtg aattgagccg ggctggtgcc ggagcgaagc ccgctggtgt tactcctgta     780

gcaacaacta ttccgattaa ttgtacgaat aaagatacag atgcggtaat gacgttggta     840

ttcgacggta acatttccgc cacacgtgat accaatggga aacaaagtat tattcaggca     900

caagataatc ctgatgttgg tattatgatt atggatagtc agcaaaactc cgtagattta     960

aatgccctgg caacatcagt aggcgttccg ttcagattgg tggaaaac                 1008
```

```
<210>    84
<211>    2592
<212>    DNA
<213>    Escherichia coli
<400>    84
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gttgtgccgc ttcttctggt tattatgcct gcatgttcaa tcgcgggaat gcgctttaac     120

cctgcttttc tgtcgggtga tactgaagct gttgctgact tatcccgctt cgagaaaggg     180

atgacttatc ttcctggtag ctatgaagtc gaagtttggg tcaatgattc ccctttactc     240

tctcgtactg taacttttaa agcagacgat gagaatcaac tgattccctg cctttcactt     300

gctgacttat taagccttgg aattaacaaa aatgcgctgc cagagcaggc tttggcttca     360
```

```
tctgaaaata gttgccttga tttgcgtatc tggtttcccg atgtgcatta catgccggag    420

ctggatgcac agagacttaa actgaccttt ccacaggcga taataaaacg tgacgctcgc    480

ggatatattc caccagaaca gtgggataac ggtattacag cttttttgct gaattatgac    540

ttttctggta ataacgatcg tggtgattac tcttcaaata actattattt aaatcttcgc    600

gctgggatca atattggtgc atggcgtttt cgcgattatt caacctggag tcgtgggagt    660

aattcagcag gtaaactgga gcatatcagt agtacgttgc agcgcgttat tattcctttc    720

agaagtgaat taacgctagg agatacatgg tcatcatcag atgttttcga cagtgttagt    780

attcgtggca taaaactgga atctgacgaa aatatgttgc ccgatagtca aagtggtttc    840

gctcccacgg tgcgcggaat tgcgaaaagt cgcgctcagg taacaatcaa acagaatggt    900

tatgtcattt atcaaaccta tatgccgccg ggaccgtttg agattagcga tcttaacccg    960

acatcatctg cgggagatct ggaagttacc atcaaagagt ctgataattc agaaactgtc   1020

tataccgtac cttatgccgc tgtccccatc ctgcaacgag aaggtcattt aaaatattct   1080

actacggttg gccaatatcg aagcaatagc tataaccaga aaagtcctta tgtatttcag   1140

ggggaattaa tttggggttt accctgggat attacggctt atggtggggc acaattctct   1200

gaggattacc gggcgttggc gctcggcctt ggcctgaatc tgggtgtatt tggtgcaaca   1260

tcgtttgatg ttactcaggc taacagttcg cttgtggatg ggagcaaaca tcaagggcaa   1320

tcttatcgtt ttctttattc caaatcgtta gttcagacag gaacagcatt ccatattatt   1380

ggctatcgtt attcaaccca gggcttttac actttaagtg atacgacata ccaacaaatg   1440

tcaggactg ttgttgatcc aaaaacgtta gatgataaag attacgttta taactggaat   1500

gattttata acttgcgtta tagcaaacgt ggaaaatttc aggctagtgt atcgcaacct   1560

ttcggtaact acgggtctat gtatttatcg gctagtcagc aaacatactg gaatactgat   1620

aaaaaagatt ctttatacca gttggttat aacaccagta ttaagggtat ctatctaaat   1680

gttgcgtgga attacagtaa atcaccaggg acaaatgcgg ataaaattgt ctcgctaaat   1740

gtctcattac ctataagtaa ttggttatct tccacgaatg atgggcgctc atcatcgaat   1800

gccatgactg caacgtatgg ttatagtcag ataaccacg gacaggtaaa ccaatatacg   1860

ggggtatctg gttctctgtt ggagcagcat aatctcagtt ataacataca acatggtttt   1920

gctaatcagg ataatagcag tagtggttct gttggtgtta attatcgtgg ggcatatggt   1980

tccttgaatt ccgcctacag ttacgataat gaaggtaatc aacaaataaa ctatggcatc   2040

agtggtgctc ttgttgtaca tgaaaatggt cttacgttga gtcaaccatt aggtgaaact   2100
```

```
aatgttttga taaaagcgcc tggagcgaat aatgtggatg ttcagcgggg gacaggaata     2160

tccactgact ggcgtggata tgcagttgtt ccttatgcaa cagaatatag acgtaataat     2220

atttcattag atcctatgtc aatgaatatg catactgaac tggatatcac ttccactgaa     2280

gttattccgg gaaaaggtgc gttagttcgt gcagagtttg ctgctcatat cggtattcgt     2340

ggtttgttca cagttcgtta tcgtaataaa tcagtcccat tcggtgctac agccagcgct     2400

cagattaaaa acagtagtca aattaccggg attgtcggcg ataatggaca actttatctc     2460

tcaggattgc ctttagaagg tgttattaat atccagtggg gagacggtgt tcagcaaaaa     2520

tgtcaggcta attacaagct ccctgaaaca gaactggata tcctgttag ctatgcaact      2580

ctggagtgcc gc                                                         2592
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<210>  85
<211>  507
<212>  DNA
<213>  Escherichia coli
<400>  85
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tccaatgctt ctgatgcttt gaaccagccg agcagtagtc taaatgatgg tgttgagact     120

ttttttattt cctgctttga tatgcctcag gaaacaacta ctgatatgga cgcttgtcag     180

agagttcagt tagctcaggt tagttgggtt aagaataagt attcggtggc cgccctgaat     240

cgtttgaaac aagacaacaa ggatgatcca cagcgtctgc aggaattaac tgcttctttt     300

aacgcggaaa gtgaagcttg dacagaatta attgagaaag cgtcaaagtc cgtccaggtt     360

gattatgtag gaggaactat agctggcact gcagttgcat cacgtcaaat tggtcttctg     420

gaattacaat cccacgatat ctgggagcac tggctacgat ctcgaggact caactcctcc     480

tcttttgcca gaaccaaagt tcaaatc                                         507
```

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<210>  86
<211>  2139
<212>  DNA
<213>  Escherichia coli
<400>  86
atggctatgt tcacaccttc attctcagga ctcaaaggtc gggcgctctt ttcactgctt      60

tttgcggcac cgatgattca tgcaacagac tctgtaacga ccaaagatgg cgaaacaatc     120

actgttacag cagatgcaaa taccgcaact gaggcaaccg atggttatca acctctgagc     180

acctccacgg cgacattaac cgatatgccg atgctggata tcccgcaggt ggtcaatacg     240
```

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gttagcgatc aggttctgga aaaccagaat gcgacaacgc tggatgaggc gctttataac    300

gtcagtaacg tggtacagac caatacatta ggcgggactc aggatgcttt tgtacgccgt    360

gggtttggcg caaaccggga tggctccatc atgaccaacg gtctgcgaac cgtacttcct    420

cgtagtttca acgccgcaac agagcgtgtg gaagtgctaa aaggcccggc ctccacgctg    480

tatggcattc tcgatcctgg cggactgatt aacgtcgtga ccaagcgccc ggaaaaaaca    540

ttccatggtt cggtttcagc cacctcctcc agttttggtg gcggcactgg gcaacttgat    600

atcacaggtc ccattgaagg cactcagctg gcgtatcgcc ttaccgggga agtgcaggat    660

gaagattact ggcgaaactt cggtaaagag cgcagtacat ttattgcccc gtcactcacc    720

tggtttggtg ataatgcaac agtaaccatg ctctattccc atcgggacta taaaactcca    780

ttcgatcgtg aacgatttt cgaccttacg acgaaacagc ccgtaaacgt tgatcgaaaa    840

atacgttttg acgaaccgtt taatattaca gatggtcagt ccgatctggc gcaactcaac    900

gcagaatatc atctcaatag ccagtggaca gcgcgctttg attacagcta cagccaggat    960

aaatacagcg ataatcaggc gcgtgttacc gcgtatgatg caacgacagg aacactgaca   1020

cggcgtgttg atgcaactca gggatctacc cagcgtatgc atgctactcg tgcggatctg   1080

caagggaatg ttgatattgc cggattctat aatgagattc tgggtggggt gtcatatgaa   1140

tattatgatc ttctgcgtac agatatgatt cgctgtaaaa aagctaaaga tttcaatata   1200

tacaaccctg tttatggtaa taccagcaaa tgtacaacgg tttcggcgtc ggacagcgat   1260

cagacgatca aacaggagaa ctactcagct tatgcacagg acgcgctcta tctgaccgat   1320

aactggattg ccgtcgccgg gatccgctat cagtattaca cgcaatatgc gggtaaaggc   1380

cgtcctttta atgtcaatac tgacagccgc gatgaacaat ggacgcccaa actggggtta   1440

gtctacaaac tgacgccatc ggtatcctta tttgccaatt attcgcaaac atttatgccg   1500

cagtcgtcaa ttgccagcta cattggcgat cttccaccag aatcatctaa tgcttacgaa   1560

gtcggggcaa aattcgagct attcgatggt atcaccgcag atattgcgct gtttgatatc   1620

cataaacgta atgtgttgta taccgaaagt attggtgatg aaaccatcgc caaaacggca   1680

ggccgcgttc gttcaagagg ggtagaagtc gaccttgcgg gagcattaac tgaaaacatt   1740

aatatcattg ccagctacgg ctataccgat gcaaaggttc tggaagatcc tgattatgca   1800

gggaaaccat tgccgaatgt tcctcgtcat accggttcgc tattcctgac ctatgatatt   1860

cataacatgc caggcaataa cacactgacg tttggcggtg cggacatgg tgtaagccgt   1920

cgttcggcaa ccaatggggc tgactattat ctgcctggct atttcgttgc cgatgccttc   1980
```

```
gccgcataca aaatgaaatt gcagtatccg gtcactctgc aattaaacgt caaaaacctg     2040

tttgataaaa cgtattacac ctcttccatc gccacaaata atctgggcaa ccagattggc     2100

gatccgcgtg aagtgcaatt cacggtgaaa atggaattt                            2139
```

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<210>   87
<211>   1818
<212>   DNA
<213>   Escherichia coli
<400>   87
atgaaaatat cgtggaatta tatatttaag aacaaatggc gatttcacat tacaagcatt      60

tcactttttc ttatcatgct cgcggtttca atcgcttttt tgcacttgcg ttttaatacc     120

ttgtccagta ccgataaaat gcggcttgaa atgtataagt ccacattata ttccaccatc     180

gagcaatttt atgttttacc ctatatgctc tcaacagacc atatcatccg tcaggcggta     240

attacgcctg acgatatgac gtccagcgaa ctcaatcaac gaattgcaca tttcaatact     300

caactcaaaa ccgcagcaat atttattctg datacccaag gtaaggccat cgcttctagc     360

aactggcagg accccggcag ctatgtaggg caaaattata gctatcgccc ctattataaa     420

cacgccatgt ctggcttaaa tggacgcttt tacggtattg gtagcactac gaatacaccg     480

ggattcttcc tctctacaag tataaaagat aaaggaaaaa ttgtcggtgt tgtagtagta     540

aaaataagtc ttaatgaaat tgaaaaagca tgggccgaag gtcctgaaaa tattatcgtg     600

aatgatgaac atgggattat atttttaagt tcaaaatcgc catggcgaat gcgaacactg     660

caaccgttac ctgttcaggc aaaacaaaaa ctacaatcta cccgccaata tagtctcgac     720

aatcttttac cggcggatta ttatccctgt tataccgtga gcaattttac tttcctgaaa     780

gataaaaaag aacaactctg tttattcccg caatattata cgcaacaaat agccattcca     840

gaatttaact ggaaaatgac aattatggtc cccttagata acctgtactg gtcatgggct     900

atttcgttag tcattacact aattatttac ctgctgtttt tgttatttat taaatactgg     960

agaatgcgat ctcatgcaca acaattatta acacttgcga atgaaacatt agaaaaacag    1020

gttaaagagc gtacatctgc cctggaattg atcaatcaaa aattaataca ggagataaaa    1080

gagcgcagtc aagctgaaca agtattacaa attacgcgta gtgaactggc agagtccagc    1140

aaactggcgg cgcttggaca gatggcaacc gaaattgccc atgaacaaaa tcaaccgtta    1200

gccgccattc acgcacttac tgataacgcg cgtactatgc taaaaaaaga gatgtatccg    1260

caggttgaac agaatctgaa acatattatt tcagtgattg agcggatgac gcagctcatt    1320
```

```
tccgaactta aagcatttgc ctcgcgccat cgcgtaccta aaggttctgc cgatgtcatc    1380

aaagtgatgt atagcgccgt ggcgttactt aatcacagca tggagaaaaa taacattgag    1440

cgacgaataa aagccccatc catgccgtta tttgtcaatt gcgatgagct cggtcttgaa    1500

cagatattca gtaatttaat tagcaacgcc ttagattcta tggaaggtag ctcttacaaa    1560

cgactggata tcgccattcg ccaggcaaat aacaaagtta ttattaccat taaagacagc    1620

ggtggcggtt ttgcacctga agttgtcgat cgcatatttg aaccattttt taccactaaa    1680

cgtagaggaa tggggttggg actggcaata gtcagcgaaa ttgtccgaaa ttcgaacggc    1740

gcactccacg ccagtaatca tcctgaaggc ggcgcagtaa tgacattaac ctggcctgaa    1800

tggggagaag aacatgaa                                                  1818
```

```
<210>   88
<211>   303
<212>   DNA
<213>   Escherichia coli
<400>   88
gtgcttacac cacaacattt acgttgtgtg ttaacatgta gcgatttact gactcttttg      60

agtggtaccg ttatgtctca aatgcccctc tattttctta atacccaaaa gaaactcact     120

gctcactatg aatggcttca aatcaacctg actgatacct acgaactagt taaaaggtta     180

atgccgattc cttcactgga cgtggtggtt aaagtaggga aacttgtcct cccggagaaa     240

gggcatcatg gttttttaccc tgaagctgga gttgtctata gaacagtagc tccagaaaat     300

cca                                                                    303
```

```
<210>   89
<211>   789
<212>   DNA
<213>   Escherichia coli
<400>   89
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gcccatgatg tctggattac aggtaaacag gcagagaaca cgttaccgc agagattggt      120

tatggtcata atttcccctc aaaggggaca attcctgaca gaagggattt ctttgaaaat     180

ccccggcttt ataacgggaa agagacaata acactgaagc cagcgtccac ggattatgtc     240

tataaaactg agtctgcaag caaagataat ggttacgttc tgtcaacgta tatgaaaccg     300

ggatactggt cgagaacctc gtcaggatgg aaaccggtca gccgggaggg cagaaatgat     360

gtggcttact gtgaatttgt cactaaatat gcaaaatctt ttattcctgg tgaacagcag     420

atgccagcac aactctatca gtctccaaca gggcatgagc ttgaaatcat tccgttatcc     480
```

```
gatataagtc gtttcagtga aaatgtgaag ctgaaagttc tgtataaaac gtccccgctc      540

gccggagcta tcatggagct tgactcggtc agttatctga catcatcccg tcatactcat      600

gcagttgagc acaaacatcc tgttcataaa gcagaactca cctttgtaac taatgaggat      660

ggtatcgtca cagtaccttc tcttcatatc ggacagtggc tggcgaaagt ccaaaataag      720

aaaagttttc aggacaaaag cctgtgtgat gaaactgtcg atgtggcaac cttaagcttc      780

tcccgaaat                                                               789
```

```
<210>    90
<211>    1134
<212>    DNA
<213>    Escherichia coli
<400>    90
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attgctatta gtgacaggga ttctacgctt tctaggttga aatcagcagg tgaaaacgga      120

gatgtagaag ctcagtatgc tttggggctc atgtatttgt atggagaaat tctggatgtt      180

gattatcagc aggcaaagat ttggtatgaa aaagccgctg accaaaatga tccgcgtgcg      240

caggccaaac tcggtgtgat gtatgcaaat ggtctcgggg taaatcagga ttatcagcaa      300

tcaaaattat ggtatgaaaa ggcggctgcg caaaatgatg ttgatgcgca atttttgctt      360

ggggagatgt atgacgatgg tctcggggta agccaagact accagcatgc aaagatgtgg      420

tatgaaaaag cggctgctca aaatgatgag cgtgctcagg tcaatctcgc tgttctatac      480

gcaaagggta atggtgttga acaggattat cgacaggcca aagctggta tgaaaaggct      540

gcagctcaaa atagtcctga tgcgcagttc gctcttggaa ttctgtatgc caatgctaat      600

ggtgtagagc aggactatca gcaggcaaaa gactggtatg agaaagcagc agaacaaaat      660

ttcgccaatg ctcagtttaa tcttggtatg ctctattaca aggtgaggg tgttaaacaa      720

aactttcggc aagccagaga atggtttgaa aaagccgcat ctcaaaatca gccgaatgcc      780

caatataatt taggtcagat ttattactac ggtcagggtg tgactcagag ctatcgacag      840

gcgaaagact ggtttgaaaa agcggcagag aaaggtcatg tcgatgctca atataatctc      900

ggtgtaaatat acgaaaatgg tgaaggtgtg agtcagaact atcaacaggc aaaggcttgg      960

tatgaaaagg cagcctcaca aaatgatgcg caggcgcagt tcgaacttgg cgttatgaat      1020

gaactgggtc agggtgaaag catagacctg aaacaagcaa gacattacta tgagcggtca      1080

tgtaataatg ggcttaagaa aggttgtgaa cggttaaaag agttattata caaa           1134
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```
<210>    91
<211>    1962
<212>    DNA
<213>    Escherichia coli
<400>    91
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aacacggtat ttgaaacgcc gtcgatggtc agtgtcgtca cgaatgacac accgtggagt     180

cagaatgcgg ttacatcggc cggcatgctg aaaggtgttg ccggtctcag ccagactggt     240

gcaggacgga ccaatgggca gacctttaat ttacgcggct atgacaaaag cggggtactt     300

gttcttgttg acggcgttcg ccaactcagt gacatggcaa aaagcagtgg cacttatctg     360

gatccggcac tcgtcaaacg tatcgaagtt gtccgcgggc caaactccag tctgtacggc     420

agtggcgggc tgggaggtgt agtggacttc agaactgccg atgcagcaga ttttcttccc     480

cccggagaga caaacggttt aagtctgtgg ggaaatatcg ccagtggtga ccacagcaca     540

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tatatccccc ctggtagata cctcgttcgt gtgcaaataa ataaaaatat gttgccacaa      240

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gaaggggcgg catttggggc agggatcctg cgcgaaccgg gagcaacaaa aaaagccgac    180

acgaaagacc tcaatgtgcc accaccggtt tatggtccgc cgcaggtgat atttcgcatt    240

gatgacaacc gctatttcac gctagaaaat tatacccact gcgagaacgg gcagacgttt    300
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aaaggccgct tattctggtt atcaacgcgt gatgattttc tggcctttcc tgccacgtta     420

aataccagac acgcttcctg tatggggtcg aataaaggct gtatgaatgc ggtcattgtc     480

actaccgatg gtggaaaaag acgcagtggt gtgccatacg gcagttatac ccagaatccg     540

accggtgcca cgagggatta tgacatgctg gtgatgaatg acggcttcta cctgcttaga     600

tatcgggggg gacagggcag atttagtccg gtgatactta gatggattct cagtactgaa     660

gatagctctg gtgttgtgcg ttcagaagat gcttatgaat tgttccgtcc cggagaagag     720

gtaccctcca ccggtttttta taaaatcgac ctgtcacgtt tttatcccaa aaacaacgtt     780

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tcgacattaa ttcaccaacg gatgcaggag gccaaggtcc cagccctttc cgtaagtgtg     180

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gccgcagaca atcgtatcct ctatgccagc ggttggttta tcgaccagaa tcaaggccct     960
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gag                                                                     1503


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cttggtcttc agctatatgg aggaatgaac tatcgcaagg aagatagtat ctctcaggga      660

acaccggcaa aagataataa gaatataacg gcaacgctcc agtttactcc gactgaaagc       720

cagaagtttg tttttgaata tggaaaaaat aaccaggtgc atacattaac acctggtgag      780

tctctcgatg cctggactat gcggggaaat cttaaacaac caaacagtaa aagagaaacg      840

cataattcac gtagtcactg ggtagcagca tggaatgccc agggcgaaat actgcatcct      900

gaaattgctg tttatcagga gaaagttatt cgtgaggtta aatcaggtaa aaaagataaa      960
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catgcagagc tccgtgatga ctcagccacg ggtaaaaaaa cgacagaaac acagtctgtt      1140

tcaattaaac agaaagctgt ttttatagaa aatgaatatg cagcaacgga ttctctcgcc      1200

ctgactggag gactgcgtct cgataatcat gaaatctatg cagttactg gaatccaaga       1260

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tcatctctga attatacggg aaaacaaatc tgggcagcac aaagaaatgg tgctaaggtt      1860

ccccgcgttc gtaatggatt cacatctatg gatattggtc taaattacca gattctgcca      1920

gacacgctga ttaattttgc cgttcttaac gtcacagaca gaaagagcga ggatatcgat      1980

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gtgtcaaata atatcctgga tgatattggt ggttataaag aaagaaatat attaatgctg      180

cgagctataa aaaaaatcat aataatgaca atcgtaaata ttatattttt ctattccttt      240

caatcgactg cggatgaaat ggtttttaata aaaaaatacg ggtttgggct tgagagagat      300

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aatcatatga attatatagc ggatgtcaat gctcaattag ctatgagtaa aaaaaataac    420

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cgcagcaggt ttaatataca ggaatcatat tgtgccatta agactaatgg tgtccttgga    180

ttcagcaacc gaaaggatgt attgcgagaa aatggtgatt caaccggaac caccagttcc    240

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gcgttaaggt ggttttctga taaacctgcc agtaccgaag aacgagggca tttctcccaa    360

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tcgataaagg tgaccatcaa ccagcaggga atacctgaag cgcagccaga cagcatgcat    480

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<213>  Escherichia coli
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ggaatggata aagcggcaaa tggtgtgccg gtcgtgaaca ttgccacgcc gaacgggggcc    180

gggatttcgc ataaccggtt tacggattac aacgtcggga aggaagggct gattctcaat    240

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ctgaaagcgg gcggggaagc gaaggctatc atcaacgaag tgaccggcgg taagcgttca    360

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aaccgtgtaa ctgcagatgg tcgtgtcaga gccctgaagg gcgaaggtga tgtgccgaaa      720

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acacaaaaaa caacgggcag gaacagcagc agtggcggtg cgtgggtgt  cagtatcggt    7680

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cacaccggag aaaaaccacc tggataccgg acgctgggtt tagtgacttt acaacgaagc    8160

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ttcatgccgt atattaagag taatttcaac cctgttactg attctgcttt gaatgtgtca     180

ctcacctata tgtatcagga tcaatatggg aaaaaacata aaaaaacatc tgaggacaga     240

tttaaaacca atcgcgatcg catagagctc tatcttaaag gttatacttt aaatagggga     300

gcatattctt tttctccttc cgcaggtttc cgttatgagt catgggatgt aaactacgat     360

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aaactcaatg accagttaag cctatatatg aatggttttg ttgcccctgt attttttaaa     480

acacaacaag agtcgagaaa agataacaat tatgtaaagg gtaagttagg ggcgaaacgt     540

tataacaacg attattatca ggaactccag attctgggtg tcagatataa atttaataat     600

gataatacgc tctgggcatc agtctataat gaaagaaaat ataatcaaca ttcctcaaaa     660
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tatgatcgct ggcaattgcg tggaggctat gattttaaag ttacagagga gtttgttttg      720

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<213>   Escherichia coli
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gttttttctg gttgtttcat ccccgcattt tcgtctccgg cagccatgct gtctccgggt      180

gaccgcagtg caattcagca gcaacagcag cagttgctgg atgaaaacca gcgtcagcgt      240

gatgcgctgg agcgcccgct gaccatcacg ccgtctccgg aaacgtctgc cggtactgaa      300

ggtccctgct ttacggtgtc aagcattgtt gtcagtgggg ccacccgact gacgtctgca      360

gaaaccgaca gactggtgcc gtgggtgaat cagtgtctga atatcacggg gctgaccgcg      420

gtcacggatg ccgtgacgga cggctatata cgccggggat atatcaccag ccgggccttt      480

ctgacagagc aggacctttc agggggcgta ctgcacataa cggtcatgga aggcaggctg      540

cagcaaatcc gggcggaagg cgctgacctt cctgcccgca ccctgaagat ggttttcccg      600

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gacatgaaga cagcactgac cggaggtctg cagcaccgca ttattcacaa ttatctggat     1140

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tggttcggcg cagaaagcga ccacgggaaa aggggagacc tgcccgtaaa tcagttccgg      1320

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actgccggac tgcctctggt ttacccggac tggcttgccc ctgaccatct cacggtttac      1740

tggcgcgttg ccgtcgcgtt t                                                 1761
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<211>  2220
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<213>  Escherichia coli
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ctgatagatt cggccaagat cggacggaat aatgcctggc ttgcaggaaa caataatttt       180

cttgaagctg gaaaatttta cactttacca acagattttt ttattgaaag ccgtggggga       240

aaaattgcta actcccatga cggtatgacc gtctttttata ctattgttcc ggttactcag      300

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tcaccagcgg gacaggaggg agctggattg tttgtcagag atattatcgg tcctcagcga       420

caggaacctc agtcagctgg aacagaagaa tatccccagg cctctaatat attgatgaat       480

gccttatta cacagaataa aaagaatgat aacttagtac agattacttc aattgttcgt        540

gaaggagtaa taaaaacatg gggtaatgaa ggtattacaa ttaagaaaca gccgatcatt       600

gagaatataa actttacgca aaaaagaaat attcatatga cgatcgagcg actaccagag       660

aagttcatcc tgaccgcttt tgataccgat cgtaaagaaa tcagtcatg gcaatttt      720

gattactcag gctttatgaa tcaactggat aataatagtt tagctattgg ttttttttgcc      780

gcacgaaatg cgaaactaag ggtgaaaaat gcatcattta aaccgggcaa gccactggtt      840

gattacaaac aattaacttc acgtcaattc agtcgtgtcc ggcataaagc ccctgaactt      900
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ctggtacagt ttccagttac tttgcaaaaa aaacataatg acttcaccgt caactttaac   1080

gttgatggga atatatcaaa aaaagctata cgcatagagc aggttaaatc aaacctgact   1140

gatccttatg agatttacgt atgtagtgat tgtcgacagg gggccagagg cagcaaaaat   1200

gaccctgtag atttacagac agccgtaaaa tttgtcgcac ccggcggtaa tatatacctt   1260

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tataaaacaa tttctgccat taatccacat aaagccattt ttataaacaa gacattcaat   1380

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aataataaac cagcatattt gcgtatagct ggtagctata atattattga gcatgtgata   1500

gccagaaata atgatgatac gggaatttct atttcagcga aagataaaaa ccgttttttc   1560

tggccagctc ataacttagt tttaaactca gattcatata ataatcttga tttatccggg   1620

attaatgccg atggttttgc tgcaaaatta ggtgtcggac cggaaacat ttttcgagga   1680

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ccaaatgcat ctgttactat tgagaattct gtagcctatg aaaatggcct gccatacaat   1800

aaagcggata tcctaaaagg gagtattggc aatggcggtg aaggtcaacc cagtaaatca   1860

caagttatta attccattgc tattaataat aatatggatg gattcactga taatttaat   1920

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ttaagaacta acccatataa attcccatca tctatccttt ttgataataa ttattcaatc   2040

agagatgatt gggaaaataa aataaaagac ttcttaggtg atacagttaa cagtgtgaat   2100

tataaattgc ttgtttcaca tgaaacagga ccggtacaaa aagatttatt tttcacacga   2160

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<213>    Escherichia coli
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acggcgaaac aagtaaaact gccaaacaac atcaaatacg ttaatactac agaggcgttt   120

tcctgtactg agattgacgg tatgaattgc cagacgaaga atccgtttaa ctataaagat   180

aacagctatg ttttcgtgct tgaacgtggt ggtgcctggt gttacgacta cactgtctcg   240
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gtacttaacc tgaaaaccgg gaaagcacag atgctcgaat acaaagacaa ccagctgtgc    300

tcaggtagca acaaaccgtt cttcgaaatc aaaaatggcg taccgacggt aggagtcatc    360

gacacatccg gaaaacctgt cgttgtggct ctggacaaac ttaaaacc                 408
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aaggggggg aatttccgga aggtttcact gatgagaaat tttccagcgc catttacaac    180

ggaagaatat ttacaatgaa acgtttacat accctgatgt tatttctggc ggttctgttt    240

actggcttta cgtggaagc agcgagcgtg aaacaagcgc tcagctgcga cccaaacgcc    300

cgggctgaac aacctggagc gtgtccaaca acgtacgagt tgtacgaagg tgacgctgcc    360

tacaaagctg cgcttgacaa agcattaaaa ccggtcggac tgagcggcat gttcggtaaa    420

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tggctccagg gcgacggttg caaagccaat acctgcggct gggactttat cgtaacactc    540

tataacccaa aaacccatga agtcgttggc taccgctact ttggtttaga tgacccggcc    600

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gtagctgcgg ttaac                                                      675
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<211>    2163
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gacaccaccg attctgccgc cggtgccggt ttcaaaacga acgatataga tgtcggcccg    180

ctgggaacga atcctggat cgaaacacca tattccagca ccactgttac taaagagatg    240

attgaaaatc agcaggcgca aagcgtcagc gagatgctga atactctcc cagtacgcaa    300

atgcaggcgc gcggtggaat ggatgtcggg cgtccgcaaa gtcgggggat gcagggcagc    360

gtggtggcca acagccgtct ggacgggctg aatatcgttt caacaaccgc gtttccggtg    420
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gaaatgcttg agcgcatgga tgtgcttaac agtttgaccg gcgcgctgta cggcccggcg    480

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gtgacgctgg gctatcaaag ccgcagtgcg tttaccggcc atgccgatct gggtggccat    600

tttgatgaaa acaaacggtt tggctatcgc gtgaacctgc ttgatcagga aggggaaggc    660

aatgtggatg acagcacgct gcgtcgcaaa ctcgtttccg ttgcgctcga ctggaatatt    720

cagccgggca ctcagctaca gctcgacgcc agccattacg aatttatcca gaaaggctat    780

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aaaaatctgg cgctcagcac tgcgggcaac gacctcacta ccgataccat cagcactcgc    900

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gaccgcgcga tgcgtagtgt ttccagtaaa atactcaaca atcagggcga tatctctcgt   1020

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gcctcaacca gcaataaaca ggttgtcggc gtgccgaaag tgcaggccaa tctgttggcg   1860

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ttc                                                              2163


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caagaaatta ccgatcgtaa ggtgatagaa gccgatctgc gtgccaccca ggacgaactg    1320

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aaagggggaat tgcggctggc atcaacgatg accaggaatg cctgtgtggt actgcaattc    1980

agactaacgg atgtggaaga tgctaag                                        2007
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ctcagcgttt ctgtcgggaa gacgaccagt gagcaggaag ctctcgagaa aacaggcgcg    180

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gccccgaaca tccaggagat gttcttctct aattcaggag gcgcatccat gaacccattc      1500

ctgaagcctg aacgtgcaga aacctggcag gcgggtttta acattgatac cagagattta      1560

ctggtcgaac aggatgccct gcgctttaag gctctggcgt accgcagcag gatccagaac      1620

tacatctaca gcgagtctta tctggtttgt tctggaggtc gtaaatgcag tctgcctgag      1680

gtgattggca atggctggga gggcattagc gatgaataca gcgacaatat gtacatctac      1740

gttaactcgg caagcgacgt tatcgcaaag ggcttcgaac tggagatgga ttatgatgca      1800

ggttttgctt ttggccgact ctctttcagc cagcagcaaa cagaccagcc aacctccatc      1860

gccagcaccc actttggcgc aggggatata accgaactgc ccagaaaata catgacgctg      1920

gatactggtg ttcgcttctt cgataacgcg ttgaccctgg gcactatcat aaaatacaca      1980

ggcaaggctc gtcgcctgtc gcctgatttt gagcaggacg aacataccgg cgcaataatc      2040

aaacaggatt tgccgcagat cccaacgatt atcgatctct atggtactta cgagtacaac      2100

cgcaacctga cactgaaact ttcggtacaa aacctgatga acagagatta ttcggaggcg      2160

ctgaataagc tcaacatgat gccaggtctt ggtgacgaga cccacccagc caattccgcg      2220

cgtggcagaa catggatatt tggcggggac attcgtttc                            2259
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<210>    118
<211>    399
<212>    DNA
<213>    Escherichia coli
<400>    118
atgtcttcga aaacaaaatg ctggctatgg atgttactgg tcatcctttc tgaaacctct        60

gcaacatcca cacttaaaat gttcgataac agtgagggga tgacaaaaac gctgctgctg      120

gccctaatcg tcgtactgta ttgcatttgt tactactcgc tttcacgggc agtaaaagat      180
```

```
atccccgttg gtctggctta cgccacatgg tccggtactg gcattttgat ggtttcaacc    240

cttgggattt tattttacgg tcaacacccg gataccgccg ccattattgg tatggtcatc    300

atagccagcg gtattatcat tatgaatctg ttctcaaaaa tgggcagtga agaggcggaa    360

gaaactccag ttaccaacct cgataaaaaa atcgctaac                          399
```

<210> 119
<211> 858
<212> DNA
<213> Escherichia coli
<400> 119

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atgtatataa aaaagcactg gatagcttta tccattctat taataccttg cattggaaac     60

gctcaggaaa ttaaaattga tgaaagctgg ttacatcaaa gcttgaatgt cattggtcgc    120

acagactctc gctttggccc aagactgact aacgacctct accctgaata tactgtagca    180

ggaagaaaag actggtttga tttttatggt tatgttgatc taccgaaatt ctttggcgtc    240

ggcagtcact atgatgttgg gatctgggat gagggctcac cactatttac ggaaatagaa    300

cctcggtttt ccattgacaa attgaccgga ttaaatcttg cgttcggccc atttaaagaa    360

tggttcattg caaacaacta tgtctatgat atgggtgaca accagtcatc ccggcaaagt    420

acatggtata tggggcttgg tacagatatc gacacgggtc taccaattaa gctttctgcc    480

aatatatacg ccaagtatca gtggcaaaac tatggtgccg ctaatgaaaa tgaatgggac    540

ggatatcgat tcaaaataaa atatagcatc cctcttacaa atttattcgg aggacgattg    600

gtatacaata gttttactaa ctttgatttt ggctccgatc ttgcggacaa gtcacacaat    660

aataaacgaa ccagtaatgc tattgcttca agccatatcc tttcccttct atatgaacac    720

tggaaatttg catttacact acgttatttt cacaacggtg gacaatggaa tgcgggagag    780

aaggttaact tcggagatgg tccatttgaa ttaaaaaata caggatgggg aacctatact    840

actattggtt atcaattt                                                 858
```

<210> 120
<211> 516
<212> DNA
<213> Escherichia coli
<400> 120

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atgagaatcg caccgcgtac cttctttgct atttccgccc tggcgtttat tgtcgcctcc     60

ggatttagtt tctggcggtt gtcccctgct gaaaatacag ggattatgag ttgttcaaca    120

aaaggcatca tgcgttttga gaatatggaa aaggagaacg ttaacggtaa tattcacttt    180

aactttggca gccagggtaa aggttcgatg gtgctcgaag ctacacgga ctctgccgct    240
```

```
ggctggctgt acctgcaacg ctatgtcaaa tttacctata ccagtaaacg tgtttccgcc        300

acggaacgcc attaccgcat cagccagtgg gaatccagcg cctcatcgat agatgaatca        360

ccagatgtga tttttgacta ctttatgcgt gaaatgtctg acagccatga cgggctgttc        420

ctcaacgccc agaagctgaa cgataaagcg attttgctca gttctattaa ttcaccgctt        480

tggatctgta cccttaaatc tggcagcaaa ttagac                                  516
```

```
<210>   121
<211>   546
<212>   DNA
<213>   Escherichia coli
<400>   121
atgaaaataa aagttatagc attggctaca tttgtttctg ctgtgtttgc tggttcagct         60

atggcctatg acggaacaat tacgtttacc ggtaaagttg tagctcagac ctgcacagtt        120

aatacaagcg acaaagactt agcagtaact ttacccactg ttgccacttc atctctaaaa        180

gacaatgctg ctacgtcagg gctgacaccc tttgccattc gtttaactgg ttgtgcaact        240

ggtatgaata gtgctcagaa tgttaaagcg tactttgagc cttcaagtaa cattgactta        300

gctacacata atttaaaaaa tactgctact ccaactaaag cggataatgt acagattcag        360

ttgctaaata gtaatggaac ttcaactatt cttttggggg aagcggataa tgggcaagat        420

gtccagtctg agacaatcgg atctgatgga agtgccacat tgcgttatat ggcccagtat        480

tatgcaacag acaatctac cgcaggggat gtaaaagcga cggtccatta taccattgcc         540

tacgaa                                                                   546
```

```
<210>   122
<211>   1077
<212>   DNA
<213>   Escherichia coli
<400>   122
atgaaaagaa tctttttcat accattgttt ttaattttac tccctaagct ggcggtagcg         60

ggtccggatg attatgtgcc ttcgcagata gcggttaata catccacatt gccaggtgtt        120

gtgattggtc ctgctgatgc ccatacctat ccccgggtga taggagagct ggcgggaaca        180

agtaaccagt atgtttttaa tggcggtgcc atcgctctga tgcgtggaaa gtttacaccc        240

gcactgccta aaattggaag tattacggta tactttccat caaggaaaca gcgtgattca        300

tctgattttg atatctatga tattggtgta tccggactgg gtattattat tggcatggcg        360

ggctattggc ccgcaacgcc tctggtcccc ataaatagct caggtatata tattgaccct        420
```

```
gtaggtgcca atacaaaccc caatacttat aacggtgcga cagcaagctt cggagctcgt      480
ttgtttgttg cttttgtcgc aacgggaaga ttacccaatg gatatataac aatacccacc      540
aggcagcttg gtactatttt gttggaagca aaacgtacaa gtttaaataa taaaggactg      600
acagcacctg ttatgttaaa tggtgggcgc attcaggtac agagtcagac atgtaccatg      660
gggcaaaaaa actatgtggt gccattaaat accgtatatc aatcacagtt cacatctttg      720
tataaagaaa tacagggagg taaaattgac atacacctac aatgcccgga tggaattgat      780
gtttatgcta cattgacaga tgcatcacag ccagtgaaca gaacagatat attgacctta      840
agcagtgaat ccactgcaaa aggatttggc atcaggctat ataaagacag tgatgtaact      900
gccatcagct atggtgaaga ctcccctgtg aaaggaaatg gcagtcaatg gcacttctcc      960
gattacaggg gagaggtaaa tccacatatc aatttaagag ccaattatat aaaaattgct     1020
gatgcaacta cacctggaag tgtgaaggct attgcaacta ttactttctc atatcaa       1077
```

<210> 123
<211> 2532
<212> DNA
<213> Escherichia coli
<400> 123

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atgaacgcta ataatctgtc atgcctgatt tactgtcgtt gttctcttct gctttttgct       60
gcattagggt taacagtaac aaaccattca tttgctgctg aagaggctga gtttgattct      120
gagttttgc atttggataa agggataaat gctattgata tccgccgctt tagtcatggt      180
aaccctgtgc ctgagggcag gtattattct gatatttatg ttaataatgt atggaagggg      240
aaggctgatt tgcagtattt acgtactgcc aataccggtg ctccgacgtt atgcctgacg      300
cctgagctgc tttcattgat tgatttagtc aaagatacta tgtcgggaaa cacctcctgc      360
tttccggcgt caacagggct ttcttcagcc agaattaatt ttgacttatc gactttaagg      420
ttgaatatcg aaatccctca ggcactgctg aatacacgtc caagaggata tatttcccct      480
gctcagtggc aaagtggtgt tcctgcagca tttataaact atgatgctaa ctattaccag      540
tatagctctt ccgggacgag taacgaacag acttatctgg gattaaaagc tggattcaat      600
ttgtggggat gggctttgcg ccaccgtggc agtgagagct ggaataatag ctatcctgcc      660
ggatatcaga atatagaaac aagtataatg catgaccttg ccccattgag agcacaattc      720
acattagggg atttttatac gaatggtgag ctaatggata gcctcagttt gcggggagtc      780
aggttagcat cggatgaacg aatgttaccc ggctctttac gtggctatgc tcctgctgtc      840
cggggaatag ctaacagtaa tgctaaagta accatttatc aaaatgctca tatcctctat      900
```

```
gaaacgacgg tgccagccgg accatttgtc atcaatgatt tatatcccag tggatatgct   960

ggtgaccttc tcgttaagat aacagagtct aatggccaga cacgaatgtt cacggttcct   1020

tttgcggccg ttgctcaact cattcgtccc ggatttagtc gctggcaaat gtcagtggga   1080

aagtatcgtt atgcgaataa aacatataat gatttaatag cacaaggcac ctatcaatac   1140

ggcctgacga atgatattac tttaaacagt ggtcttacca cagcttcagg atatacagcg   1200

gggttagctg gcctggcctt taatacccct ctgggtgcta tagcatctga cattacattg   1260

tccagaacag cattcaggta ttccggtgta acgcgtaaag gttatagtct gcactcaagt   1320

tatagcatca atattccagc ctcaaacaca aatataactc tggcggctta tcgttattca   1380

tcaaaagatt tttatcatct gaaggatgcg ctatcagcta atcacaacgc gtttattgat   1440

gatgtttctg taaaaagtac agcgttttat cgtcccagga atcaattcca gatttcaatc   1500

aaccaggaat taggtgaaaa atggggtggg atgtatttaa caggaacaac ctataattac   1560

tggggacata aaggaagtcg taatgaatac cagattgggt acagcaactt ctggaaacaa   1620

ctcggctatc aaattggatt gtctcagtca agagataatg agcaacaacg ccgtgatgac   1680

agattttata ttaattttac tctccctctg ggaggaagtg ttcaaagccc ggtgttttcc   1740

actgttttaa attatagcaa agaagagaaa aatagtattc agacatcaat tagtggtact   1800

ggcggggagg ataatcagtt ctcttatggt atttcaggaa acagccagga aaacgggcct   1860

tccggttatg caatgaatgg gggttatcgt tcaccttatg taaatataac cacaacagtc   1920

gggcatgata ctcagaataa taatcaaagg tcatttggtg cgtcgggagc ggtggtcgca   1980

cacccctatg gagtgacatt gagtaatgac ctgagtgata cttttgccat tatccatgct   2040

gaaggagctc aggggctgt catcaataat gcctctggta gtcgtctgga tttttgggga   2100

aatggtgttg ttccttatgt tacaccctat gagaaaaatc aaattagcat cgatccctcc   2160

aatttagatt tgaatgttga attatcggcg acggagcagg aaatcattcc tcgtgctaat   2220

agcgccacgt tagtgaaatt tgacactaaa acaggaagaa gtctgttatt tgatattcgt   2280

atgtctactg gcaatccccc tccaatggct tctgaagttc tggatgaaca tggacagttg   2340

gccggatatg tcgctcaggc cgggaaggta tttaccaggg gactccctga aaaaggtcat   2400

ctcagcgttg tatggggacc agataataaa gacagatgtt catttgtata tcatgttgca   2460

cacaataaag atgatatgca atctcagctc gttcctgttc tgtgtataca gcaccctaat   2520

caggaaaaaa ca                                                       2532
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<210>   124
<211>   831
<212>   DNA
<213>   Escherichia coli
<400>   124
atggtaaaat gtcatactct gattaaccgt agaaataaat gtctgctgat tgttttttata       60

gtccttattg gatggattat attcagacct aaagcatata cttattcact aaatgataaa      120

gaaaaagaga tgctcataat gttatcacaa catcctgaaa ctcggtactt tggatttttat      180

tccatagaac ttccggctga ttacaaacca acaggaatgg ttatgttcat acaaggatcg      240

gcgatgatcc ctgtagaaac aaagctacaa tattatcctc cttttctgca atatatgaca      300

cgatatgagg cagaactaaa aaacacctca gcattagatc cactggatac gccttatttg      360

aagcaagttc acccactaag tccacctatg aatggagtca tttttgaacg aatgaaagcg      420

aaatacaccc cagattttgc acgagtattg gatgcatgga atgggaaaa tggcgttacg      480

ttttcagtaa aaatagaagc taaagatggt agagcaaccc gctatgatgg aattagtaag      540

attgccgaat acagttatgg atataatatt ccagaaaaaa aagtacagtt acttactatt      600

ctttcaggac tacaacctcg tgcagataac caaccccat cagaaaataa attggcgata      660

caatatgcac aggttgacgc ttcactactt ggagagtatg aattatctgt agattataaa      720

aatagcaata atattaaaat aagtttgcag acggataata atagttatat tgactcatta      780

ttagatataa gatatccgag taatggaaac agagcatggt ataactctat a             831


<210>   125
<211>   1098
<212>   DNA
<213>   Escherichia coli
<400>   125
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ggtactctgt ttattttatc ggtctggaat tctgcgacat actgggatat ttttattttat      120

ggcgttctgc caatgctgtt tctttggcta tgtttgtttg gtattgcgct gaacaaatat      180

gaacaatccg ttgcagcctg tataagttgg gagtctgaaa gacaacaagt taaacaactc      240

tggcaacact ggagccaaaa acaactggca atagttggga atgttctttt tacaccggaa      300

gaaaaaggca tgagtgtttt actggggcca caggaagaga tccctgcata tcctaaaaag      360

gcacgaccgt tattctctgc atcccgttat tctctttcgt ctatattcca tgatattcac      420

cagcaactga cacaacaatt tcctgattat cgtcattatc tacatactat ctacgtatta      480

cagcctgaga atggcgtgg agaaaccgtg agacaggcta ttttccatca atgggactta      540
```

```
gtacctgaac ggaccaatac tcttaatcaa atccagtctc tttatgatga aagatttgac     600

ggtctaattc tggttgtttg tttacaaaac tggccggaga ataaacctga agatacgagt     660

gaactggtat cagcacagct tatctcctca tcgtcatttg tacggcagca ccagataccc     720

gttattgctg gtctggggcg tgtaatgcca ttagaacccg aggagttgga gcataatctg     780

gatgtgttat ttgaatataa ccaattggat aacaaacaac tacagcatgt ctgggtctct     840

ggtttagatg agggaacgat agaaaacctt atgcagtatg ctgaacaaca tcaatggtca     900

cttcctaaaa aacggcccct acacatgatt gatcattcct ttggccctac aggagagttt     960

attttcctg tctctctggc aatgctgtca gaggctgcca agaaactga acaaaatcat    1020

ttaattatct atcagtcagc acagtatgct cagaaaaaga gcctttgcct gattacccgg    1080

aagctttatt taaggaca                                               1098
```

```
<210>   126
<211>   780
<212>   DNA
<213>   Escherichia coli
<400>   126
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tccatcatta tcaataacac cgtacgttca tttcagaggt cagtcatgaa taccagagct     120

cttttttccc tgctgttcac tgtggcatca ttctccgcct ccgccggcaa ctgggctgtc     180

aaaaacggct ggtgtcagac catgacggaa gatggtcagg cgctggtaat gctgaaaaat     240

ggcacgattg gtattaccgg cctgatgcag ggatgcccga atggtgtaca gacgctcctg     300

ggcagccgta tcagtattaa cggtaacctg atccccacat cacaaatgtg taatcagcag     360

acgggattca gggctgttga ggtggaaatc ggacaggcgc cggaaatggt caaaaaagcc     420

gttcactcca tagcagagcg tgatgtgtcc gttttacagg catttggtgt acgaatggaa     480

ttcacccgcg gtgatatgct gaaggtctgt ccgaaatttg tcacatcact tgccggtttt     540

tccccgaaac agacgaccac tattaataaa gattccgtcc tgcaggctgc ccggcaggca     600

tacgcccggg aatatgacga ggaaacaaca gaaaccgctg attttggctc ttacgaagta     660

aaaggcaata aggttgagtt tgaagtattc aatcctgaag accgtgcgta cgacaaagtg     720

accgtcacgg ttggtgctga cggtaatgcc accggcgcca gcgttgaatt tatcggaaaa     780
```

```
<210>   127
<211>   1155
<212>   DNA
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<213>  Escherichia coli
<400>  127
gtggtaatta tcaatagcac gatactgagc ggcgcaggcg ctatcccttc cctgacgtcg      60

ctcttacccg acatcagaaa aatgctgctg gtcactgacc gtaatattgc gcagctcgac     120

ggtgtgcagc agattcgcgc cttactggaa aagcactgcc cgcaggttaa cgttatcgat     180

aatgtgcccg cagagcccac gcatcatgat gtgcgccagc taatggatgc ccctggcgat     240

gcctcttttg atgtggtggt cgggatcggc ggtggcagcg tgttggatgt ggcgaagctg     300

ctatcggtgc tttgccatcc acaatcaccg gggctggatg cgctgcttgc gggtgaaaaa     360

ccgactcagc gggtgcaatc atggttgatt cctacaaccg ccggaaccgg ctcagaagcc     420

acgccgaatg cgattctggc aatccctgag caaagcacga aggtgggtat tatttcccag     480

gtgctgttac cagactatgt ggcgcttttc ccggaactga ccaccagcat gcccgcgcat     540

attgcggcgt ccacgggcat tgatgctctt tgccacttac tggagtgttt taccgcgacc     600

gtggcaaatc cggtcagcga taacgcggcg ctgactgggt taagtaaact tttccggcac     660

attcaacccg ccgtgaacga tcctcaggat ctgcgcgcaa aactggaaat gctgtgggcg     720

tcttactatg cggcgtagc gataacccat gcgggcacgc atctcgttca tgcgctctcc     780

tacccgttag gtggcaaata tcatctgccg catggcgtcg cgaatgccat cttgctggcg     840

ccgtgcatgg cgtttgttcg cccctgggcg gtcgagaaat ttgcccgggt ctgggattgc     900

attcccgatg cggaaaccgc cctgagcgcg gaagaaaaat ctcatgccct ggtgacctgg     960

ttacaggcat tagtcaatca actcaagcta cccaacaatc tcgcggctct cggcgtaccg    1020

ccagaggata ttgcctctct gagcgaggcg gcactgaacg tgaagcgcct tatgaacaat    1080

gtgccgtgcc aaattgatct acaggacgta caggccattt accaaacact gtttccgcaa    1140

catccattta aggag                                                     1155


<210>  128
<211>  315
<212>  DNA
<213>  Escherichia coli
<400>  128
atgaatatca gaaaactgtt ttgtccggga aacacccccc ggattttatt gttttttattc      60

ttttttgttg tttctgcaat aaccacaatt gcatgcggat acactgagaa gaatgcaaca     120

ggaaatgtgc tgcttctgtt tctccttctg ctccttgcac acagaaatac cctcacatcc     180

attacagcgc tgttatttct gttctgttgt gcactgtatg cgcctgccgg tatgacgtac     240

ggtaaaatca caacagtttt tattgtcgcg ttgttgcaga ccacaactga tgaggcagcg     300
```

gagtttaccg ggatg   315

<210>   129
<211>   441
<212>   DNA
<213>   Escherichia coli
<400>   129
atgaatattc aggcaataaa agaaatggta aatttaattt gtagtttttt atttatattc   60

tttctgtcct cggctttttgt ttcttttggg tgttatgcta tttatgaatt gtttttatgg   120

aatgatatta ttgtatatag ctggggatat atattaattg tcttttttacc tttcacatta   180

tatgtaatgt cgtttgagat tttgttttttt gctattagtg ggcgacgatt gtctaaagta   240

acaatggtgc gcctttggtt gataattaaa attattattg ctttctctat ttgcgcagtg   300

ttgattttttt cttcaatttta caaaaaagaa ttattatcta gaaattatat tgcttgtagt   360

ggtatcccgt ctgggtggat gccgggtctg gcaacgaaat acgttaaaga aaaatcatta   420

tgcgaaaaaa atggcaataa t   441

<210>   130
<211>   534
<212>   DNA
<213>   Escherichia coli
<400>   130
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ctgagtggct gcgggctgat tcagaaagtg gtggatgaat cgaaaagcgt ggcctcagcc   120

gttttctaca aacaaatcaa aatactgcat ctcgatttct tctcccgcag cgccctgaat   180

acggatgcgg aagatacgcc gctttccacg atggtgcatg tctggcaact gaaaacccgc   240

gaagattttg acaaggcgga ttacgacacc ctgtttatgc aggaagagaa gacgctggag   300

aaggacgtac tggcaaaaca caccgtctgg gtaaaaccgg aaggcacggc atccctgaat   360

gtgccgctgg ataaagagac gcagtttgtc gccattattg ggcagtttta tcaccctgat   420

gaaaaaagcg acagctggcg tctggtgatc aaaagggacg aactggaggc cgacaagccg   480

cgctcgattg aactgatgag aagcgacctg cgactgctgc ctctcaagga taaa   534

<210>   131
<211>   627
<212>   DNA
<213>   Escherichia coli
<400>   131
atgttcttaa aaagaaaatg gtattacgca gtgacgacat ctgtcgtcat tactttgtgt   60

215

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ggtggaggat attatatgta caggcaagaa tatcagatgg ttgtcactgt accaactgct      120

gacgcgaacg atcccaactg gccaaataaa aggatacagt ttgataccag cgaatggcta      180

cagcaacttc aatatattaa aatagatgat cattatatat tgaatactca atatactcca      240

attgctaatt tggatgactt tggtattaca ttaaaattac agaacgcatt aaatgggtcg      300

gataaaagac ttcctgcact atatggcctt gctgagatgg atgctcagaa atttaaagac      360

ctgatgcgcg gtaaaattaa atgtgaatat ctgaggacga catttgatgc ggaaacatta      420

aagcctgtca atgattattt ccttatttct tttacttata aagataagtg gtatgaattt      480

gagacagaaa gaaaaatatc taaaacaagt gatgatgggt atttttgtg ggcatttgat      540

aatactgtcc acgaagcagg ctattggcat aacacagatc cggctgcgta ttcctataga      600

gattaccaga atggtaaggc tgtgaaa                                         627


<210>   132
<211>   1272
<212>   DNA
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Seq ID 153

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TTATCGTCAGGAACAACATCCGGGTGGCGCGACGACGGGCTTCCCGCAAGCAAAAATCGATTTTAGCTCTGGTTGGCTAC
AAGATGAGATCACCTTACGCGATCTGCCGATTACCCTGCTTGGCGGAACCCGCTATGACAGTTATCGCGGTAGCAGCGAC
GGCTACAAAGATGTTGATGCCGACAAATGGTCATCTCGTGCGGGGATGACTATCAACCCGACCAACTGGCTGATGTTATT
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TCTATACCAACTATTGGGTGCCAAACCCGAACTTACGTCCGGAAACTAACGAAACTCAGGAGTACGGTTTTGGGCTGCGT
TTTGATGACCTGATGTTGTCCAATGATGCTCTGGAATTTAAAGCCAGCTACTTTGATACCAAAGCGAAAGATTATATCTC
CACGACCGTCGATTTCGCGGCGGCGACAACTATGTCGTATAACGTCCCGAACGCCAAAATCTGGGGCTGGGATGTGATGA
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ATCTCCAGCATTAACCCGGATACCGTTACCAGTACCCTGAATATTCCGATCGCTCACAGCGGCTTCTCTGTTGGTTGGGT
CGGTACGTTTGCCGATCGCTCAACACATATCAGCAGCAGCTACAGCAAACAACCTGGCTATGGTGTGAATGATTTCTACG
TCAGTTATCAAGGGCAGCAGGCGCTCAAAGGCATGACCACTACTCTGGTATTGGGCAACGCCTTCGATAAAGAGTACTGG
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Seq ID 154

ATGAGGGATGAAATGTTATATAATATACCTTGTCGAATTTATATCCTTTCCACTCTGTCATTATGCATTTCTGGGATAGT
TTCTACTGCAACCGCAACTTCTTCAGAAACAAAAATCAGCAACGAAGAGACGCTCGTCGTGACCACGAATCGTTCCGGCAA
GCAACCTTTGGGAAAGCCCGGCGACTATACAGGTTATTGACCAACAAACATTGCAGAACTCCACCAATGCCTCCATAGCC
GATAATTTGCAGGACATCCCCGGAGTAGAGATAACAGACAACTCCTTGGCAGGCCGTAAACAAATCCGCATTCGTGGCGA
AGCATCCTCCCGTGTTTTAATTCTCATTGATGGTCAGGAGGTAACTTATCAGCGCGCCGGAGATAATTATGGTGTGGGAC
TGTTGATAGATGAGTCTGCGCTGGAGCGTGTTGAGGTAGTGAAAGGTCCATATTCCGTACTGTACGGTTCACAGGCAATT
GGCGGTATTGTTAACTTCATAACCAAAAAGGGGAGGTGACAAACTTGCATCTGGAGTTGTGAAAGCTGTTTATAATTCCGC
AACAGCAGGCTGGGAAGAATCAATCGCGGTCCAGGGGAGCATCGGTGGATTTGATTATCGCATCAACGGTAGTTATTCTG
ATCAGGGCAATCGTGATACGCCGGATGGACGTCTGCCGAATACCAACTATCGTAACAATAGTCAGGGTGTATGGTTGGGT
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CGGAAGCTATGAGGCATTTAGTGTCAAAATACCTAAACTTGAACGAGAGAAAGTTGGGGTATTCTATGACACAGACGTGG
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ACACAGCCTGTTCCCAGTCCGATGATTCAGGCTCTGACCGTTCATAACAAGACTGACACCCATGATAAGCAATACACTCA
GGCGGTCACATTGCAGAGTCACTTTTCGCTGCCTGCTAATAATGAACTTGTTACCGGTGCACAGTACAAACAAGACAGGG
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CACATACGGAAATCCTGATCTTAAGGCTGAACACTCCAATAACTTTGAATTAGGTGCACGATATAATGGTAATACGTGGC
TGATTGACAGCGCAGTTTACTACTCAGAAGCTAAAGATTATATTGCAAGTCTGATCTGTGATGGCAGTATAGTTTGCAAT
GGTAACACCAACTCCTCCCGTAGTAGCTACTATTATTATGACAATATTGATCGGGCAAAAACATGGGGACTGGAAATAAG
CGCGGAATATAATGGCTGGGTTTTCTCGCCATATATCAGTGGCAATTTAATTCGTCGGCAATATGAAACTTCAACATTAA
AAACAACTAATACAGGAGAACCAGCGATAAACGGACGTATAGGGCTGAAACATACTCTTGTGATGGGTCAGGCCAACATA
ATCTCTGATGTTTTTATTCGTGCTGCCTCTAGTGCAAAGATGACAGTAACGGTACCGAAACAAATGTTCCGGGCTGGGC
CACTCTCAACTTTGCAGTAAATACAGAATTCGGTAACGAGGATCAGTCCCGGATTAACCTAGCACTCAATAACCTGACAG
ACAAACGCTACCGTACAGCACATGAAACTATTCCTGCAGCAGGTTTTAATGCAGCTATAGGTTTTGTATGGAATTTC

Seq ID 155

ATGCGTAAAGTTTGTGCAGTCATTTTGTCCGCAGCCATCTGTCT
GTCCGTATCCGGTGCGCCTGCATGGGCGTCTGAACATCAGTCCACACTGAGCGCGGGGTA
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CCGTTATGAGTTTACGGACGCGCTGGGGCTGATTACGTCCTTCAGTTATGCCAATGCTGA
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GATGGCGGGTGTGGCTTACAGCCGTGTGTCGACTTTCTCCGGGGATTATCTCCGCGTAAC
TGACAACAAGGGGAAAACGCACGATGTGCTGACCGGAAGTGATGACGGTCGCCACAGCAA
CACGTCTCTGGCGTGGGGGGCTGGCGTGCAGTTTAACCCGACCGAATCCGTGACCATTGA
CCTTGCTTATGAAGGTTCCGGTAGTGGCGACTGGCGAACGGATGCATTTATTGTTGGTAT
CGGATACCGTTTCTGA

Seq ID 156

ATGAAAAAATCGACATTATCTTTAGCCATCGGTTTATTATTGGCATGTAGTACCGGTATGGCAAAAACACAGCATTTAAC
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CTCGATAACTGGTATTTTGAATTAAACACGTTACTGGAAGACGGAACATCTTTATATAACGACGGTAATTATCATGGACG
CGATATGGAACAGCAGAAAAATGTTGCTTATCTGCGTCCGGTAATTGCCTGGTCGCCGACGGAAGAATTCACCGTTTCCG
CAGCGATGGAAGCGAATGTGGTAAATAATGCTTATGGTTATACCGATAGCAAGGGTAATTTTGTCGATCAGTCCGATCGT
ACCGGTTATGGCATGAGTATGACCTGGAATGGCCTGAAAACCGATCCGGAAAATGGCATCGTGGTTAATCTTAATACCGC
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ACTTCTTC

Seq ID 157

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CGGACAGCAACCTGACGGCGGATGGCGAAGCCGCGCCGGTGGATGTCCAGTTGGTTTATCTGAGCGACGACTCAAAATTC
CATGCCGCCGACTACGACCAGGTTGCCACCACCGCGCTGCCCGACGTGCTGGGGAAAAACTATATCGATCACCAGGACTT
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Seq ID 158

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GGCGTACTGACCACTCCCGGCGGGGATGATCTGCTCCGCCGCCGCCTGCGCGAACACTGGCTGGGCTGGCTGATGCAAAC
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CATGTGGATACCGAAGATAACCCGTTCACCGGCGGTCTGTTCAGCCTGTTCCGTTTACCGGATACGTTGTAT
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(54) Title: EXPEC-SPECIFIC PROTEINS, GENES ENCODING THEM AND USES THEREOF

(57) Abstract: The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of: 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria, 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates, 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates, 4- testing the polypeptides for immunogenicity using animals models. Application for making vaccines compositions and immunotherapies

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C12N15/63 C07K14/245 C07K16/12 A61K39/108
G01N33/53

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 66572 A (INST NAT SANTE RECH MED ;NASSIF XAVIER (FR); TINSLEY COLIN (FR); B) 13 September 2001 (2001-09-13) SEQ ID NOs:390 and 391 page 3, line 20 - page 4, line 17 page 29, line 23 - line 31	1-6, 9-13,15, 16
A	JOHNSON JAMES R ET AL: "Phylogenetic and pathotypic similarities between Escherichia coli isolates from urinary tract infections in dogs and extraintestinal infections in humans." JOURNAL OF INFECTIOUS DISEASES, vol. 183, no. 6, 2001, pages 897-906, XP002211433 ISSN: 0022-1899 abstract	

-/--

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 August 2003	0 5. 12. 2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Mata-Vicente, M.

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MUEHLDORFER I ET AL: "Characterization of Escherichia coli strains isolated from environmental water habitats and from stool samples of healthy volunteers." RESEARCH IN MICROBIOLOGY, vol. 147, no. 8, 1996, pages 625-635, XP002211434 ISSN: 0923-2508 table I page 630, paragraph 2 -----	

INTERNATIONAL SEARCH REPORT

Box I   Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)   –

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

   see FURTHER INFORMATION sheet PCT/ISA/210

2. [X] Claims Nos.:   14
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

   see FURTHER INFORMATION sheet PCT/ISA/210

3. [ ] Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

   see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

   1-6, 9-13, 15 and 16 partially

Remark on Protest
    [ ] The additional search fees were accompanied by the applicant's protest.

    [ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

Continuation of Box I.1

As far as an "in vivo" method is concerned, claim 9 is directed to a
method of treatment of the human/animal body and the search has been
carried out and based on the alleged effects of the
compound/composition.

As far as an "in vivo" method is concerned, claim 15 is directed to a
diagnostic method practised on the human/animal body and the search has
been carried out and based on the alleged effects of the
compound/composition.

Continuation of Box I.2

Claims Nos.:   14

Claim 14 refers to "monoclonal antibodies against epitopes of
polypeptide", but it does not say which polypeptide is meant. In
consequence, the scope of said claim is ambiguous and vague and its
subject-matter is not sufficiently disclosed and supported (Art. 83 and
84 EPC). Therefore, no search has been carried out on said claim.

The phrase "polypeptide such as used according to claim 9" comprised in
Claim 13 lacks any sense. Nevertheless, the ISA has assumed that it is
an error and that it refers to the polypeptides referred to in Claim 9
or, in other words, a polypeptide selected from the group comprising SEQ
ID NOs:1-66 (except SEQ ID NO:8) and 133-145.

The applicant's attention is drawn to the fact that claims relating to
inventions in respect of which no international search report has been
established need not be the subject of an international preliminary
examination (Rule 66.1(e) PCT). The applicant is advised that the EPO
policy when acting as an International Preliminary Examining Authority is
normally not to carry out a preliminary examination on matter which has
not been searched. This is the case irrespective of whether or not the
claims are amended following receipt of the search report or during any
Chapter II procedure. If the application proceeds into the regional phase
before the EPO, the applicant is reminded that a search may be carried
out during examination before the EPO (see EPO Guideline C-VI, 8.5),
should the problems which led to the Article 17(2) declaration be
overcome.

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

This International Searching Authority found multiple (groups of)
inventions in this international application, as follows:

Invention 1: Claims (1-6, 9-13, 15 and 16) - partially

> Isolated antigenic polypeptide SEQ ID NO:14; the
> polynucleotide encoding it (SEQ ID NO:80); vector comprising
> said polynucleotide and host cell transformed with it;
> antibodies against said polypeptide; vaccines comprising the
> polypeptide; methods of diagnosis/treatment derived of the
> use of any of the molecules previously mentioned.
> ---

Inventions 2-32: Claims (1-6, 9-13, 15 and 16) - partially

> Idem as invention 1, but restricted to each one of the
> polypeptides of SEQ ID NOs: 15, 17, 21-23, 28-30, 32, 36,
> 38, 39, 41-44, 46, 49, 50, 52-55, 58, 60, 63 and 133-138 and
> their corresponding genes (SEQ ID NOs:81, 83, 87-89, 94-96,
> 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119 and
> 126).
> ---

Invention 33: Claims (4-6) - partially

> Isolated polynucleotide SEQ ID NO:127, vector comprising it
> and host cell transformed therewith.
> ---

Inventions 34-41: Claims (9-13, 15 and 16) - partially

> Idem as invention 33, but restricted to each one of the
> polynucleotides SEQ ID NOs: 130, 132 and 146-151.
> ---

Invention 42: Claims (9-13, 15 and 16) - partially

> Use of the polypeptide SEQ ID NO:1 as antigen; vaccines;
> antibodies against said polypeptide; methods of
> diagnosis/treatment derived of the use thereof.

> ---

Inventions 43-86: Claims (9-13, 15 and 16) - partially

> Idem as invention 42, but restricted to each one of the
> polypeptides SEQ ID NOs: 2-7, 9-13, 16, 18-20, 24-27, 31,
> 33-35, 37, 40, 45, 47, 48, 51, 56, 57, 59, 61, 62, 64-66,
> 139-145.

> ---

Invention 87: Claims (7 and 8) - completely

Process for isolating and identifying polypeptides useful as
vaccines comprising the steps of: selecting on the basis of
sequence analysis those of the polypeptides which are either
located in the outermembrane or secreted by the bacteria;
identifying the genes coding for said polypeptides which are
conserved in B2/D clinical isolates; purifying the
polypeptides identified in step 1, which are found in step 2
to be conserved in B2/D isolates; and testing the
polypeptides for immunogenicity using animal models.

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 0166572	A	13-09-2001	FR	2806096 A1	14-09-2001
			CA	2402602 A1	13-09-2001
			WO	0166572 A2	13-09-2001
			EP	1328641 A2	23-07-2003
			US	2003148324 A1	07-08-2003